



HUMAN TELOMERASE

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGGCGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCGCCGCCCTCCTCCGCCAGGTGTCCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGGAAGAACGTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGGACGGGCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCGTGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCAGCTGCGCCTACCAGGTGTGGGGCCCGCGCTGTACAGCTGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCTGCCAGCCCCGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240

Fig. 1A



GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGCTGGGCCACCGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCACGCCGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCGGTGTACGCCGAGACCAAGCACCTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCCGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCAGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGGCGGGCCCCGGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGTCGCTGGTGAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGCGGGCTGCCTGCCGGCTGGTGCCCCAGGCCTCTGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAAACGAACGCCGCTTCAGAACACCAAGAAGTTCATCTCCCTGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500

Fig. 1B



CAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTGGCTG AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	1560 520
CGCAGGAGCCCAGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCTGCACTGGCTGATGAGTGTACGTGAGCTGCTCAGGTCTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
TTTATGTACGGAGACCACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTC PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	1740 580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCAGTTGAAGAGGGTGCAGCTGCAGGAG TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTCGGAAGCAGAGGTCAAGCAGCATCGGGAGCCAGGCCGCCCTGCTGACGTCCAGA LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	1860 620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	1980 660
CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGCGCCTCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	2040 680
CTGGGCCTGGACGATATCCACAGGGCTGGCGCACCTCGTGCCTGCGTGTGCAGGGCCAG LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	2100 700
GACCCGCCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTCACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGC ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	2220 740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTCAAG ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	2280 760

Fig. 1C



AGCCACGTCTTACCTTGACAGACCTCCAGCGTACATGCGACAGTCGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCGCTGAGGGATGCCGTCGTACAGCAGAGCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTCTCGACGTCTCCTACGCTTGTGCCACCGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCCGGGATTCCGGCGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	2580 860
GGGCTGCTCCTGCGTTGGATGATTCTTGTGGTACACCTCACCTCACCCACGCG GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	2640 880
AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTAACTTG LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	2700 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAACGAGGCCCTGGGTGGCACGGCTTTGTT ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	2760 920
CAGATGCCGGCCCACGGCCTATTCCCTGGTGCAGCCTGGATACCCGGACCCCTG GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	2820 940
GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCACCTC GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	2880 960
AACCGCGCTTCAAGGCTGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGCAGGCTG AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	2940 980
AAGTGTACAGCCTGTTCTGGATTGAGGTGAACAGCCTCCAGACGGTGTGCACCAAC LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	3000 1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCA IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	3060 1020

Fig. 1D



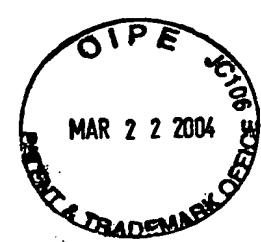
TTTCATCAGCAAGTTGGAAGAACCCACATTTCTGCGCGTCATCTGACACGGCC PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	3120 1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	3180 1060
GCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGCCACCAAGCATTCTGCTC AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	3240 1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	3300 1100
ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn	3360 1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTgatggccacccgcccacagccag ProAlaLeuProSerAspPheLysThrIleLeuAsp	3420 1132
Gccgagagcagacaccagcagccctgtcacgcgggctctacgtcccgaggaggaggg Cggcccacaccaggccgcaccgctggagactgaggcctgagtgagttggccgag gcctgcattgtccggctgaaggctgagtgtccggctgaggcctgagcagtgccagccaa gggctgagtgtccagcacacctgcccgtcttcaacttccacaggctggcgctcgctcca ccccagggccagctttcctcaccaggagccggctccactccccacataggaaatagtc catccccagattcgcattgttcacccctgcgcctgccttcacccac catccaggtggagaccctgagaaggaccctggagctctggaaattggagtgaccaaag gtgtccctgtacacaggcgaggaccctgcacctggatggggccctgtggtaaaatt ggggggaggtgctgtggagtaaaatactgaatatatgagttttcagtttggaaaaaaa aaaa	3480 3540 3600 3660 3720 3780 3840 3900 3960 3964

Fig. 1E



Euplotes	1	-----MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIWKVIRCR--NQSQSHYKOLEDIR
HT1	1	RRLGPQGWRLVQRGDPAFRALVAQCLVCVPWDAR-PPPAAPSFRQVSCLKEVARVLQRLCERGAKNVLAFCFALLGA
EST2	1	-----MKILFEFIQDKLDID--LQTNSTYKENLKCG
Euplotes	56	IFAQTNIVATPRDYNEEDFKVIARK-----EVFSTGLMIELIDKCLVELLSSSDVSDRQKLQCFGQLKGNC-LAK
HT1	80	RGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDDVLVHLLARCALFVLPAPSCAY--QVCGPPLYQLGAATQA
EST2	30	HFNGLDEILTT-CFALPNSRKIALP-----CLPGDLSHKAVIDHCIYLLTGEYNN--VLTFGYKIARNEDVNN
Euplotes	126	THLLTALSTQKQYFFQDEWNQVRAMIGNELFRHLYTKYLIFQRTSEGTLVQFCGNVFDHLKVNDKFDKKQKGGAADMNE
HT1	157	RPPPHASGPRRLGCRCAWNHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRRGAPEPERTPVGQGSWAHPGRTRG
EST2	97	SLFCHSANVNVTLLKGAAWKMHSVLGTYAFV DLLINYTVI QFNGO-FFTQIVGNRCNEPHLPPKVVQRSSSS-----
Euplotes	206	PRCCSTCKYNVKNEKDHFLLNNI-----NVPNWNMKSRTTRIFYCTHFNRRNNQFF
HT1	237	PSDRGFVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRRPPWDTPCPPVYAEKHFLYSSGDK--EQLR
EST2	169	---SATAAQIKQLTEPVVN-----KQFLHKLNNIN-SSSFF
Euplotes	255	KKHEFVSNKNNISAM-DRAQTIFTNI-----FRFNIRKKLKDKVIEKIAYMLEVKDFNFNYYLTKSCPLPENWRE
HT1	315	PSFLLSSLRPSLTGARRLVTIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVP
EST2	200	PYSKILPSSSSIKKLTDLREAIFP-----TNLVKIPQRLKVRINLTQKLLKRHKRLNYVSILNSICPPILEGTL-----
Telomerase domain		
Euplotes	326	RK----QKIENLINKTREEEKS--KYYEELFSYTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKKYELNKHE
HT1	394	AAGVCAREKPQGSVAAPEEEETDPRLVQLLRQHSSPQWQVYGFVRACRLRVPPGLWGSRHNERFLRNTKKFISLGKHA
EST2	268	-----VLDLSHLSRQ-----SPKERVLKFIIVILOKLLPQEMFGSKKNKGKIIKNLNLLSLPLNG
Euplotes	398	LIHKNLLLEKINTREISWMQVET-SAKHFYYFDHENIYVWKLLRWFEDLVVSLIRCFFYVTEQQKSYSKTYYRKNIW
HT1	474	KLSLQELTWKMSVRDCAWLRRSPGVGVCPAAEHLREEILAKFLHWLMSVYVVELLSFFYVTETTFQKNRLFFYRKSVW
EST2	324	YLPFDSSLKKLRLKDFRWFISD-IWFTKHNFENLN-QLAICFISWLFRQLIPKIIQTFYCTEIS-STVTIVYFRHDTW
Motif 1 Motif 2		
Euplotes	477	DVIMKMSIADLKK-ETLAEVQEKEVEEWKSL-GFAPGKLRLIPKTT--FRPIMTFNKKIVNSDRK--TTKLTNTKLL
HT1	554	SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG--LRPIVNMDYVGARTFRREKRAERLTSRK
EST2	401	NKLITPFIVEYFK-TYLVENNVCRNHNSYTLS-NFNHSKMRIIPKKSNNEFRIIAIPCRGADEEFT--IYKENHKNAIQ

Fig. 2A



Motif A

Euplotes 551 NSHMLKTLKN-RMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLSS
HT1 632 ALFSVLNYERARR--PGLLGASVGLDDIHRAWRTFVLRVRAQDPPPFLYFVKVDVTGAYDTIPCDRLTEVIASIICKPQN
EST2 477 PTQKILEYLRNKRPTSFTKIQSPTQIADRIKEFKQRLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDAKNN

Euplotes 629 DFWIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTIVEAK-CRNYFKK
HT1 710 TYCVRRYAVVQKAHGHVRKAFKSHVS-----TLTDLQPYMRQFVAHLQETSPLRDAVIEQSSSLNEASSG
EST2 556 GFFVRSQYFFN-TNTGVLKLFNVVN-----A--SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIFKT-

Motif B

Euplotes 708 NLLQPVINICQNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
HT1 777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIPQGSILSTLLCSCYGDME-----KLFAGIRRD-----GLLLRLVDDFLLVT
EST2 616 --ALWVEDKCYIR-----EDGLFQGSSLAPIVDLVYDDLLEFYSEFKASPSQD-----TLILKLAODFLIIS

Motif C

Euplotes 788 TQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIQDYZCDWIGISIDMKTALMPNINLRI
HT1 847 PHLTHAKTFLRTLVRGVPEYGCVNLRKTVNFPVEDEALGG-TAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYAR--
EST2 677 TDQQ-QVINIKKLAMG-----GFQKYNANRDKILAVS-----SQSDDDTVIQFCAMHIFVKELEVWKHSSTMW--

Euplotes 868 EGILCTLNLNMQTKKASMWLKKLKSFLMNNIHYFRKTITTEDFANKTLNKLFIISGGYKYMQCAKEY--KDHFKKNLAM
HT1 924 TSIRASLTFRNGFKAGRNMRRKLFVRLKCHSLFLDLQVNSLQTVCNTIYKILLLQAYRFHACVQLQPFHQVWKNPFT
EST2 741 -----NFHIRSKSS---KGIFRSILALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINVTO

Motif D

Motif E

Euplotes 946 SSMIDLEVKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIIEIFSTKLYIFNRVCMILKAKEAKLKSDOCQS
HT1 1004 FLRVIISDTASLCYSILK4KNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLKLTRHRVTYVPLLGSRTAQTLSRKLPGT
EST2 808 NMQFHSFLQRRIEMTVSG---CPITKCDPLIEYEVRI--FTI--LNGFLESLSSNTSKF-KDNIILLRKEIQLQAYIYI

Euplotes 1026 LIQYDA-----
HT1 1083 TLTAALEAAANPALPSDFKTIID
EST2 879 YIHIVN-----

Fig. 2B

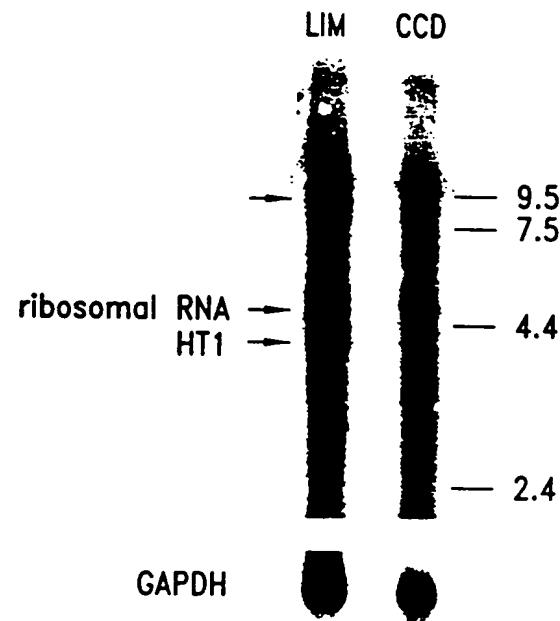


Fig. 3



Plasmid	Human blood					LIM1215						
10	5	1	H	E	P	X	B	H	E	P	X	B

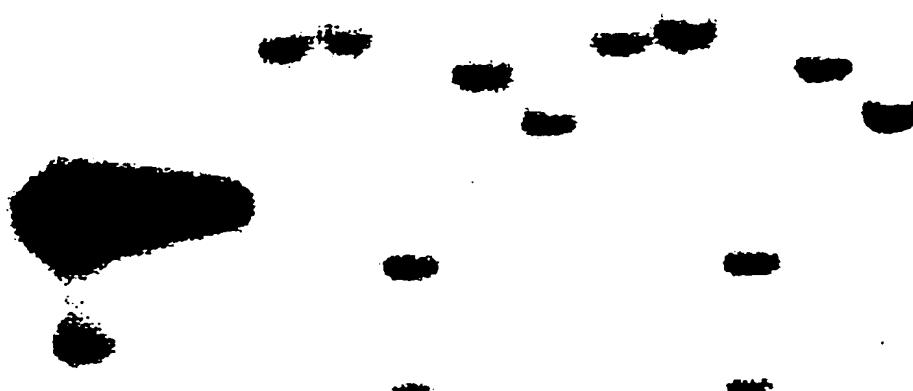


Fig. 4

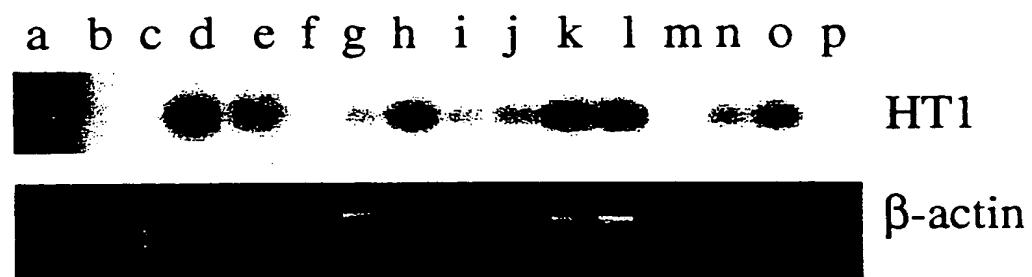


Fig. 5

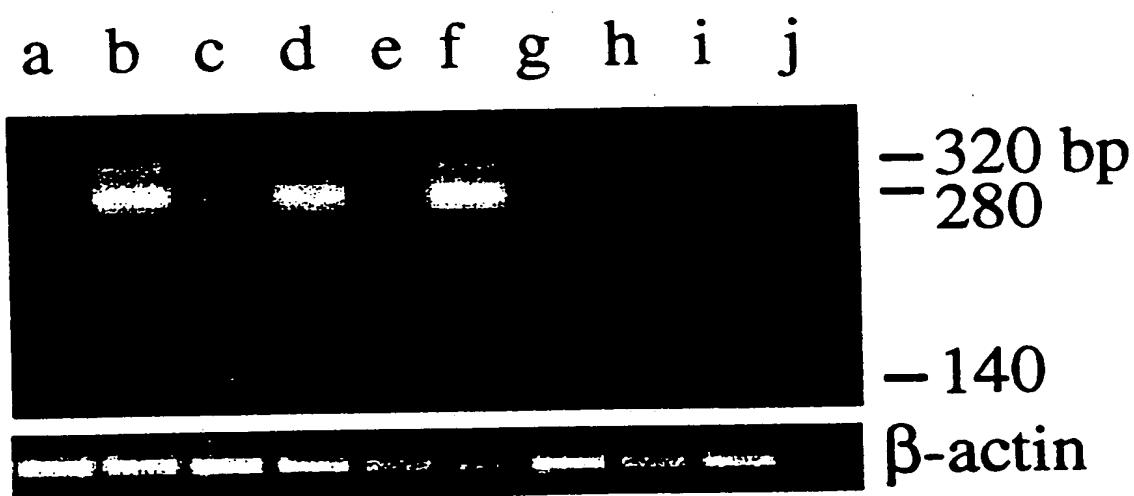


Fig. 6

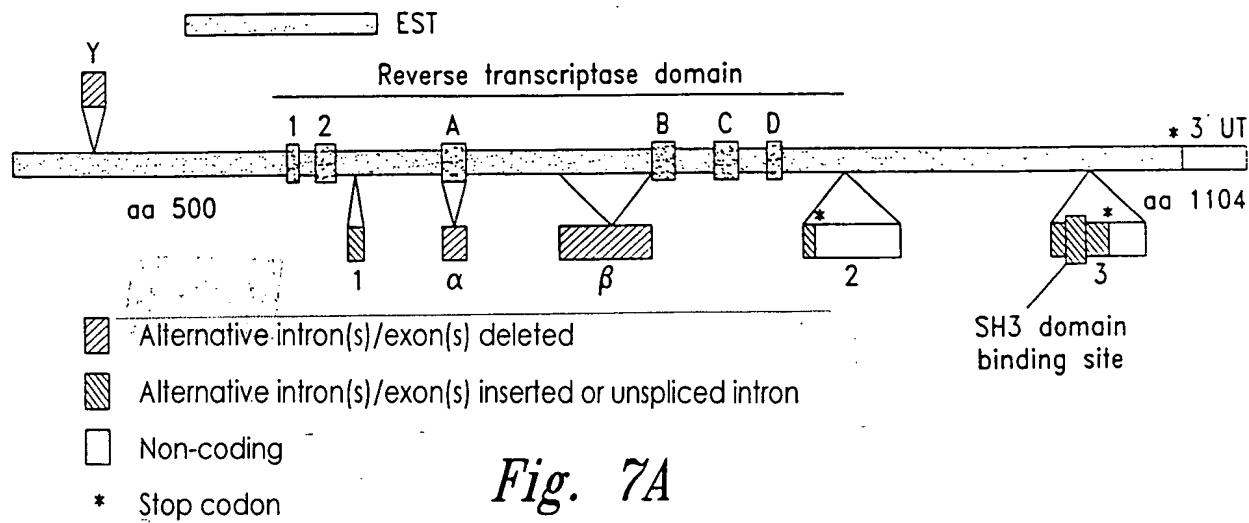


Fig. 7A

Variants:	1	α	β	2	3
RT-PCR product	NO	+	+	NO	+ & -
PCR from LIM1215 lib.	-	+	-	+	NO
RT-PCR product	NO	-	+	NO	+
53.2 cDNA	-	-	-	-	NO

Fig. 7B



	222	223
Y	5'-CCAGGTG ggcctc	gcaggtg TCCTGCC-3'
	1950	1952
1	5'-AAAGAGG GTGGCTG.....	AACAGAA GCCGAGC-3'
	2130	2167
a	5'-TGTCAAG gtggatg.....	cccccag GACAGGC-3'
	2286	2468
b	5'-GAGCCAC gtctcta.....	ggggcaa GTCCTAC-3'
	2843	2844
2	5'-ACTCCAG GTGAGCG.....	XXXXXXX CTATGCC-3'
	3157	
3	5'-AACGCAG CCGAAGAAAACATTTCTGTCGTGACTCCTGCCGTGCTTGGTCGGGACAGCCAGAGATGG T A A E E N I L V V T P A V L G S G Q P E M E AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTCCGGTGTCTCCTGGGAGGGAGTTG P P R R P S G V G S F P V S P G R G V G	
	3158	
	GGCTGGGCCTGTGACTCCTCAGCCTCTGTTTCCCCAG GGATGTC-3'	
	L G L *	

Fig. 7C



a b c d e f g h i j k l



- 430 bp
- 400
- 250
- 220

Fig. 8

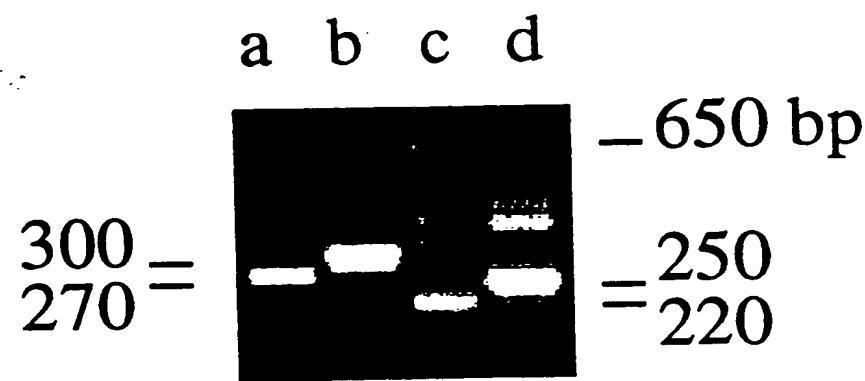


Fig. 9

MAR 22 2004

sequence "Y" 104-105 bases
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACCA
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly* GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases
GTGGCTGTGCTTGTTAACCTCCTTTAACAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence " α " 36 bases
GTGGATGTGACGGGCGCGTACGACACCATCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence " β " 182 bases
GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu
CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTACAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeu
AATGAGGCCAGCAGTGGCCTTCGACGTCTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis
GCCGTGCGCATCAGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGAG
Ter

GGCGTTCGTCACCTCTGCTTCCGTGTGGGGCAGGCAGTGCATGCCAATCCAAAGGGT
CAGATGCCACAGGGTGCCCTCGTCCATCTGGGGCTGAGCACAAATGCATCTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTCTGTGCTATTTGGTAA...



sequence "3" 159 bases

CCGAAGAAAACATTCTGCGTGACTCCTGCGGTGCTTGGGTGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCTGTGACTCCTCAGCCTCTGTTTCCCCAG
GlyValGlyLeuGlyLeu *

sequence "X" unknown length

...GACAGTCACCAGGGGGTTGACCGCCGGACTGGCGTCCCCAGGGTTGACTATAGGA
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTAGAGGCCTGGCTGGCATGG
GTGGACGTGGCCCCGGCATGGCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
CACTGAGTCGGTGGGGCTTGTGGCTCCCGTGAGCTCCCCCTAGTCTGTTGTCTGG
CTGAGCAAGCCTCCTGAGGGGCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)

GTGGCTGTGCTTGGTTAACTTCCTTTAACAGAAGTGCCTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCACCCATTGTGCGCACAGTGAGGTGGCCGAGGTGCCGTGCCTCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGCAGGGAC....

Fig. 10B



Truncated telomerase

ATGCCGCGCCTCCCCCTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGGCCCCAGGGCTGGCGCTGGTCAGCGGGGACCCGGCGCTTCCGCGCTGGGCCAGTGCCTGGTGTGGCTGCCCTGGACGCACGGCCGCCCCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCTCTCCGCCAGGTGCTCTGCCAGGGACTGGTGGCCAGTGCAGAGGCTGTGGAGGCCGCGAAGAACGTGCTGGCCTCGCCTGCTGGACGGGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGACGCAGTGCAGGGAGCGGGCTGGGGCTGCTGCAGGGCAG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTACCTGCTGGCACGCTGCCCTTGTGCTGGCTCCAGCTGCCCTACAGGTGCTGGGCCGCGCTGTACAGCTGGCCTGCCACTCAGGGCAG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCCTGGCCTGCCAGCCGGTGCAGGGAGGGCAG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGCTGCCGTTGCCAACAGGGCCAGGCGTGGCACGCCAGCCGAGCTGCCAGGGTCCGGCCACCCGGCAGGAGCGTGGACCGACTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCCGAACAGGCCACCTCTTGAGGGTGCCTCTGGCACGCCACTCCACCCATCGTGGCCGCCAGCACACGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCACCGTCCCTGGACACGCCCTGCCCCGGTACGCCAGAACACTCTACTCTCAGGCACAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTGAGGCCAGCCTGACTGGCCTCGGAGGCTGTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGACTCCCCCAGGTGCCCTGCCAGGCC
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGTGCCCTACGGGTGCTCTCAAGACGACTGCCGCTGCCAGGTGCCCTGCCAGGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAACCCCAAGGGCTGTGGCGCCCCGGAGGAGGACACAGACCCGGTGGCAGCTGCCCTGGCAGCTGCCCTGGCAGGTGACGGCTCGTGG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCTCCAGGCCAACGAACGCCCTCCCTAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAAG
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGCAAGATGAGCGTGGGACTGCCCTGGCTGCCAGGAGCCAGGGTGGCTGTTCGGCCAGAGCACCGCTGCCAGGTGAGGAGATCTGCCAAG
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTACGTGTCAGCTGAGCTGCTCAGGTCTTCTTATGTCAGGAGACCGTTCAAAGAACAGGCTTTCTACCGGAAGAGTGTGGAGCAAG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AAT--NNN--GACAGTCACCAGGGGGTTGACCGCCGACTGGCGTCCCCAGGGTGA
CTAGGACCGGTGTCAGGTGCCCTGCAAGTAGAGGGCTCTAGGGCGTCTGGCTGG

Fig. 11A



CATGGGTGGACGTGGCCCCGGGATGGCCTTCTGCCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGCTGGGGCTTGTGGCTTCCGTGAGCTTCCCCTAGTCTGTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTATTC...

Fig. 11B



Truncated protein 1

ATGCCGCGCGCTCCCCGCTGCCAGCGCGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCCACGTCG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGGCCCCAGGGCTGGCGCTGGTGAGCGCGGGACCCGGCGTTCCCGCGCTGGTGCCAGTCGCTGGTGTGCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCTCTTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGCCCGAGTGCTGCAGAGGTGTCGAGCGCGCGGAAGAAC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACCTGCTGGCACGCTGCCGCTTTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCCGCTGCTACAGCTGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTGGGATCGAACGGCTGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGCCTGCCAG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAAGAGGCCAGGGCTGGCTGCCCTGAGCCGGAGCCGCTGGCAGGGTCTGGCCACCCGG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGCTGGTGTACCTGCCAGACCCGCCAGAGGCCACCTCTTGAGGGTGCCTCTGGCACGCCACTCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCACACGCCCTGGACACGCCCTGTCGCCAGAACGACTCCCTACTCC
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCCAGCCTGACTGGCGCTGGAGGCCATCTTGAGGGTCCAGGCCCTGGATGCCAGGGACTCCCG
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTCTGGAAACACGCCAGTGCCCTACGGGCTCTCAAGACGCACTGCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

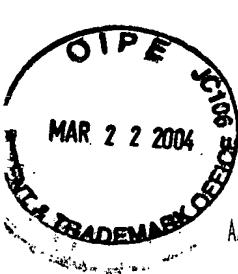
GGAGAAGCCCCAGGGCTCTGTCGGCGCCCCGGAGGAGGAGACACAGACCCCGTCCCTGGCAGCTGCC
E K P Q G S V A A P E E E D T D P R R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCCCTCAGGACAACGAACCCCGCTCTCAGGA
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGGCGAGAGCACCG
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGAGCTGCTGAGCTGCTCAGGTCTTCTTATGTCACGGAGACCA
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11C



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCCGGAGCTGTCGGAAAGCAGAGGTCAAGCAGCATCGGGAAAGCCAGGCCGCCCTGCTGACGTCAAGACTCCGCTTCATCCCCAAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTGGTTAACCTCCCTTTAACCGAGAA
V A V L W F T F L F N Q K

CGGGCTGCCCGATTGTGAACATGGACTACGTCTGGGAGCCAGAACGTTCCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G *

Fig. 11D



Truncated protein 2

ATGCCGCGCGCTCCCCCTGCCAGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCCTGGGGCCCAGGGCTGGCGCTGGTCCAGCGCGGGACCCGGCGCTTCCCGCGCTGGTGGCCAGTGCTGGTGTGCGTCCCTGGGACCCACGGCCGCCCCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGCTGTGCGAGCGCGCGGAAGAACGTGCTGGCCTCGGCTGCGTGGACGGGGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCCCGAGGCTTACACCAGCGTGGCAGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGCTGCTGCTGCCCGTGGCGACGAGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACGCTGGCGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGCGGCCGCGCTGTACCAAGCTCGGCCTGCCACTCAGGCCGGCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCGTGGGATGCGAACGGCCTGGAACCATAGCGTACGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCCGGTGGGAGGAGCGGGGGAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGCGTGGCGCTGCCCTGAGCCGGAGCGACGCCGTGGCAGGGTCTGGCCACCCGGCAGGACCGCTGGACCGAGTGCACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAACAGCCACCTCTTGAGGGTGGCTCTGGCACGCCACTCCACCCATCGTGGCCGCCAGCACCGGGCCCC
G F C V V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACACGCTCCGGACACGCCCTGTGCCCTGGTACGCCAGACCAAGCACTTCTCTACTCTCAGGCACAAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGTGGAGACCATCTTCTGGGTCAGGCCACTCCCGCAGGGACTCCCCGAGGTGCCCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCAAGCGCAGTGCCCTACGGGTGCTCTCAAGACGCACGCCCTGGCAGGTGACGGTGTGGCTGCCAGCGCTACTGGC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGGCGCCCCGGAGGAGGAGACACAGACCCCGCTGGCAGCTGCCAGCACAGCAGCCCCGGTGTACGGCTCGTGGCGCT
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P H Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCAGGCCCTGGGCTCCAGGACAACGACGCCCTCCAGGAACACCAAGAACGTTCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAAGATGAGCGTGGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGTCTGGTGAAGAGATCTGGCCAAGTTCTGCACGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTCTTATGTCACGGAGACCAAGCTTCAAAGAACAGGCTTTTACCGGAAGAGTGTGAGGAGCAAGTGCACGGCT
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11E



AATCAGACAGCACCTGAAAGAGGGTGCAGCTGCCGGAGCTGTCCGAACGAGGTCAAGCCATCGGGAAGCCAGGGCCGCCCTGCTGACGTCCAGACTCCGTTATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R O H R E A R P A L L T S R L R F I P K P D
CGGGCTGCCGCCGATTGTGAACATGGACTACGTCGTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGTCTCACCTCGAGGGTGAAGGCAGTGTAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGCGCCGCCGCCGCCCTCTGGCGCCTCTGTCTGGCCTGGACGATATCCACAGGGCCTGGCGACCTTCGTGCTGCGTGTGCGGCCAGGACCCCCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAGGTGGATGTGACGGGCGCTACGACACCATCCCCAGGACAGGCTCACGGAGGTCACTGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGATGCCGTGGTCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V O
GAAGGCCGCCATGGCACGTCCGAAGCCTTCAAGAGCCAC
K A A H G H V R K A F K S H

GTCTTACGTCCAGTG
V L R P V

CCAGGGATCCGCAGGGTCCATCTCTCCACGCTGCTGCAGCCTGTCTACGGGACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGGCTGCTCTGCGTTGGGGA
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G
TGATTTCTTGTGGTACACCTCACCTCACCCACCGGAAACCTCTCAGGACCTGGTCCAGGTGTCCCTGAGTATGGCTGCCGTGGTAACCTGGGAAGACAGTGGTAACTTCC
*

Fig. 11F



Reference protein

ATGCCGCGCCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGCTTCCGCGCCTGGTGGGCCAGTGCCTGGTGTGCGTGCCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCCCGCCGCCCTCCTCCGCCAGGTGTCCCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCGAGTGCAGAGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCCTGCTGGACGGGGCCCGGGGGCCCCGAGGCCTTCACCACCAAGCGTGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCACTGCAGGGGAGCGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlyAlaTrpGlyLeuLeu	140
TTGCCTGGCGTGGCGACGACGTGCTGGTCACCTGCTGGCACGCTGCGCCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCAGCTGCCCTACCAAGGTGTGCGGGCCGCCGCTGTACAGCTCGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCGAAGCGTCTGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCGGGGGCAGTGCCAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGTCTGGGCCACCCGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACCGCTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300

Fig. 11G



CGCCAGCACCACGCCGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCGGTGTACGCCGAGACCAAGCACCTCCCTACTCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCGAGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGCCCCGGAGAACGCCCAGGGCTCTGGCGGCCGGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGCAGGCCCTGCCTGCGCCGGCTGGTCCCCCAGGCCTCTGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
GCCAAGCTCGCTGCAGGAGCTGACGTGAAAGATGAGCGTGCGGGCTGCGCTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
CGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCGCTGCGTGAGGAGATC	1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle	540
CTGGCCAAGTTCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC	1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
TTTATGTCACGGAGACCACGTTCAAAGAACAGGCTTTTCTACCGGAAGAGTGTC	1740
PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGCAGCTGCGGAG	1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
CTGTCGGAAGCAGAGGTCAAGGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCCAGA	1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620

Fig. 11H



CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG	1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA	1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
CTGTTCAGCGTGCCTCAACTACGAGCGGGCGCGCCCGCCCTCCTGGCGCCTCTGTG	2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGTGCGTGTGCGGGCCAG	2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
GACCCGCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC	2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
CCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGC	2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCATGGCACGTCCGCAAGGCCTTCAAG	2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
AGCCACGTCTCACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGTGGCTCACCTG	2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
CAGGAGACCAGCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCCTGAATGAG	2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	800
GCCAGCAGTGGCCTTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATC	2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG	2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTGCCGGGATTGCCGGGAC	2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
GGGCTGCTCCTGCCTTGGATGATTCTTGGTGCACACCTCACCTCACCGCG	2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGTAGAACAGACGAGGCCCTGGGTGGCACGGCTTTGTT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCCACGGCCTATTCCCTGGTGCAGGCTGCTGGATAACCCGGACCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940

Fig. III



GAGGTGCAGAGCGACTACTCCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCACCTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AAACCGGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGC GGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCTGTTCTGGATTTGCAGGTGAAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCA	3060
IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

Fig. 11J

TRADEMARK

Truncated protein 3

ATGCCGCCGCTCCCCCTGCCAGCCGTGCCTCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCGTGGCACGTTCTG
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

 CGGGCCCTGGGGCCCAGGGCTGGCGCTGGTGAGCGCGGGGACCCGGCGCTTCCGCGCGCTGGTGCCCCAGTGCTGGTGTGCCGTGCCCTGGGACGCACGCCGCCCGCC
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

 CCCCCTCTCCGCAGGTGCTCTGCCGAAGGAGCTGGTGCCCCAGTGCTGCCAGAGGTGCTGCCAGGCCGAAGAACGTGCTGCCCTGGCCTGCCGTGGACGCCGCCCG
 P S F R Q V S C L K E L V A R V L Q R I C E R G A K N V L A F G F A L L D G A R

 CGGGGGCCCCCGAGGCCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACGCCGGGAGCGGGCTGGGGCTGCTGCCGTGGACGCCG
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

 GCTGGTCACCTGCTGGCACGCTGCCCTTTGCTGGCTCCAGCTGCCACAGGTGCTGCCCTGCTACAGCTCGGCGCTGCCACTCAGGCCGGCC
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

 ACACGCTAGTGACCCGAAGGGCTGGGATGCAACGGCCTGGAACCATAGCTCAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCCCGGGTGGAGGGAGGCCGG
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

 CAGCCGAAGTCGCCGTGCCAACAGGGCCAGGCCTGGCGCTGCCCTGAGCCGGACCGACGCCGTGGCAGGGCTCTGGGCCACCCGGCAGGACGCTGGAC
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

 TGGTTCTGTGTTGTCACCTGCCAGACCCGCCAGAGCCACCTTTGGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTGGCCGCCAGCAC
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R O H H A G P P

 ATCCACATGCCGCCACACGCCCTGGACACGCCCTGCCCCGGTACGCCAGACCAAGCACTCCCTACTCCCTAGCCACAAGGAGCAGCTGCC
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

 CCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGTTGGAGACCATCTTCTGGGCTCAGGCCCTGGATGCCAGGACTCCCCCAGGTTGCC
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

 AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCCAGCTGCC
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

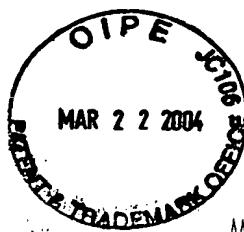
 GGAGAAGCCCCAGGGCTCTGGCGGCCCGAGGGAGGAGACACAGACCCCGTGCCTGGTGAGCTGCCAGCACAGCAGGCCCTGGCAGGT
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

 CCTGCCGCCCTGGTCCCCAGGCCCTGGGCTCCAGGACAACGAACGCCCTCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCC
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

 GACGTGGAAGATGAGCGTGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGGCGAGAGCACCGCTGCCAGGGAGAT
 T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

 GATGAGTGTGACGTGTCAGCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTGGAGCAAGT
 M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S T G

Fig. 11K



AATCAGACAGCAGCTTGAAGAGGGTGCAGCTCCGGGACCTGTCGGAAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCAAGACTCCGCTCATCCCCAAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTCCGCCATTGTGAACATGGACTACGTCTGGGACCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTAAGGCAGTGTCAAGCTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
CGGGCGCCGCCGGCCCTCTGGGCCCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGACCTTCGTGCTCGTGTGCGGGCCAGGACCCGCCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGCAAGGTGGATGTGACGGCGCGTACGACACCACCCAGGACAGGCTCACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCCTGGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCGCCCATGGCACGTCGCAGAGCCTCAAGAGCCACGTCACCTGACAGACCTCCAGCCATACGCGACAGTTGTGGCTACCTGCAGGAGACCAGCCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGTGTATCGAGCAGGCTCCCTGAATGAGGCCAGCAGTGGCTTCGACGTCTTACGTTATGTGCCACCCCTGCGCATCAGGGCAAGTCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCGCAGGGCTCATCCTCTCCACGCTGCTGCAGCCTGTGCTACGGGACATGGAGAACAGCTGTTGGGGATTGGCGGGACGGCTGCTCTGCCTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R O G L L R L V D
TGATTTCTTGTGGTACACCTCACCTACCCACGGAAAACCTTCTCAGGACCCCTGGTCCGAGGTGCTGAGTATGGCTGCGTGGTAATTGCGGAAGACAGTGGTGA
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGAGAAGACGAGGCCCTGGTGGCACGGTTTGTCAAGATGCCGCCACGGCTATCCCTGGTGGCTGCTGGATACCCGGACCTGGAGGTGAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R
GTGAGCGCACCTGGCGGAAGTGGAGCCTGTGCCGGCTGGGCAGGTGCTGCAGGGCGTTGCGTCCACCTCTGCTTCCGTGGGGCAGGGACTGCCAATCCAAAGGGTCA
*
TGCCACAGGGTCCCCCTGTCCATCTGGGCTGAGCACAAATGCACTTCTGTTGAGGTGAGGGTGCCTCACACGGGAGCAGTTCTGCTATTTGGTAA.....

Fig. 11L



Altered C-terminus protein

ATGCCGCGCGCTCCCCGCTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGGTGTGCCCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCCGCGCTGGTGGCCAGTGCTGGTGTGCCCTGGGACGCACGGCCGCCCCCGCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCTCTTCCGCCAGGTGTCTGCCAGAGCTGGTGGCCAGTGCTGCAGAGCTGTGCAGAGCGCGCGCAAGAACGTGTGCCCTCGGCTCGCCTGGACGGGGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D O G A R

GGGGGGCCCCCGAGGCCCTCACCAACAGCGCTGCCAGCTACCTGCCAACACGGTGACCGACGCAGTGGGGAGCGGGCTGGGGCTGTGTGCGCCCGTGGCGACGAGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCCGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGTGCCGCGCCGTGTACCAAGCTGCCGTGCCACTCAGGCCGGCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTGGGATGCAACGGCCTGGAACCATAGCGTAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCCGGGTGCGAGGAGGCAGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGCGCTGCCGCTGCCCTGAGCCGGAGCGACGCCGTGGCAGGGTCTGGCAGGGCCACCCGGCAGGACCCGTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAAGAGCCACCTCTTGAGGGTGGCTCTGGCACGCCACTCCACCCATCCGGCCGGCCAGCACACCGGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACACGCTCCGGACACGCCCTGTCGGGAGACCATCTTGAGGGCTCTGGCACGCCACTCCCTACTCAGCGACAAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCCTGACTGGCGCTGGAGGGCTGTGGAGACCATCTTGAGGGCTCTGGCACGCCACTCCCGAGGTGTGCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAAACACGCCAGTGCCAGTGCCCTACGGGGTCTCTCAAGACGCAGTGGCGAGCTGCCCTGGATGCCAGGGACTCCCGCAGGGTGTGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

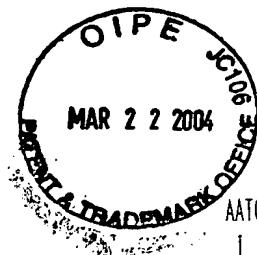
GGAGAAGCCCCAGGGCTCTGTGGCGCCGGAGGGAGGAGACACAGACCCCGTCCCTGGTCAGCTCTGCCAGCACAGCAGGCCCTGGAGGTGTACGGCTCTGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCTCCAGGACAACGAACGCCCTCCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGGCCAGGGTGGCTGTGCTGCCAGAGCACCGTCTGCCAGGAGATCCTGGCAAGTTCTGCACTGG
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTACGTGTCAGCTGCTGGCTTCAGGCTTTATGTCAGGAGACCAAGCTTCAAAGAACAGGCTTTTACCGGAAGAGTGTGAGGACAGTTGCAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11M



AATCAGACAGCACTGAAGAGGGTGCAGCTCGGGAGCTGCGAACAGAGGTCAAGGAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTCATCCCCAAGGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGGGGCCATTGTGAACATGGACTACGTGGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGTCTCACCTGAGGGTGAAGGCAGTGTCAAGCGTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGGCGCCGCCGGCCCTCTGGGGCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAGGTGGATGTGACGGGCGCTACGACACCATCCCCAGGACAGGCTCACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCCTCGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCGCCCATGGGACGTCGCAGAGCCCTCAAGAGGCCACGTCACCTGACAGAACCTCCAGCCATCGCACAGCTGCGTGTGCGTACCTGCAGGAGACCAGCCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGTGTATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCTGGCTCTCGACGCTTACGTTGACAGACCTCCAGCCATCGCACAGCTGCGTGTGCGTACAGGGCAAGTCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCCGAGGGCTCATCCTCTCCACGCTGCTGCAGCTGTACGGGACATGGAGAACAGCTGTTGGGGATTGGGGACGGGCTGCTCTGCCTGGTGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L R L V D
TGATTCTTGTGGTGAACCTCACCTCACCCACGCAGAACCTTCTCAGGACCTGGTCCAGGTGCTGAGTATGGCTGCGTGGTAATTGCGGAAGAACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGTAGAAGACGAGGCCCTGGTGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGCAGGCTGCTGGATACCGGACCTGGAGGTGCAAGCTGACAGCCCTGGAGGTGCAAGACACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S
CTATGCCGGACCTCCATCAGAGCCAGTCACCTCAACCGGGCTCAAGGCTGGAGGAACATGCGTCCAACTCTTGGGGTCTGGCTGAAGTGTACAGCCCTGGAGGTGCAAGACACTCCAG
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D
TTGAGGTGAACAGCCTCAGACGGTGTGACCAACATCTACAAGATCCTCTGCTGAGGTACAGCATGTTGCTGAGCTCCATTICATCAGCAAGTTGGAGAA
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H Q Q V W K N
CCCCACATTTCTGGCTATCTGACACGGCTCCCTGCTACTCCATCTGAAAGCCAAGAACGAGGTGCTGGGGCAAGGGCCGCCCTGCCCTGGAGGTGCAAGACACTCCAG
P T F F L R V I S D T A S L C Y S I L K A K N A E
CCGAAGAAAACATTCTGCGTACTCCTGGGTGCTGGTC
E E N I L V V T P A V L G S
GGGACAGCAGAGATGGAGCCACCCCGCAGACCGTGGGTGAGCTTCCGGTCTCTGGAGGGAGTTGGCTGGCTGTGACTCCTCAGCCTGTTCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11N



Protein that lacks motif A

ATGCCGCCTCCCCCTGCCAGGCCGCTCCCTGCTGCCAGCCACTACCGCAGGGTGTGCCCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCCGCGCTGGTGCCCCAGTGCTGGTGTGCCCTGGGACCCACGGCCGCCCCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCCGCCAGGTGTCTGCCAGAGCTGGTGCCCCAGTGCTGCCAGGGCTGTGCCAGGCCGCGAAGAACGTGTGCCCTCGCTGCCGCTGGACGGGGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACAGCGCTGCCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGGCCGGCTGGGGCTGTGTGCCCGCTGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCCCTGGCTCCAGCTGCCCTACAGGTGTGCCGGCCGCCGTGTACCAAGCTGCCACTCAGGCCCTGCCACTCAGGCCGGCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTGGATGCAACGGCCTGGAACCATAGCTCAGGGAGGCCGGTCCCCCTGGCTGCCAGCCCCGGTGCAGGAGGCCGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGGGCTGCCAGGGCTGCCAGGGCTCTGGGGCTCTGGCACGCCACTCCACCCATCCGGCCGCCAGCACACGCCGGCCCC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAGAACGCCACCTCTTGAGGGTGTCTCTGGCACGCCACTCCACCCATCCGGCCGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H A G P P

ATCCACATGCCGCCAACACGCTCTGGACACGCCCTGTGCCGGTACGCCAGAACACTTCTCTACTCCCTAGCGACAAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGGCTGTGGAGACCATCTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGGC
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCAAGGCCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGCAGCCGTCTGTGCC
M R P L F E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCAGGGCTCTGTGGCGGCCAGGGAGGGACACAGACCCCGTGCCTGGTGCAGCTGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTCTGTGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGGCTGGTGCCTGCCAGGCCCTGGGTCTCCAGGACAACGAACGCCCTCCAGAACACCAAGAACGTTCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC
L R R L V P P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGCCAGGGTGGCTGTCTCCAGAACACCAAGAACGTTCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

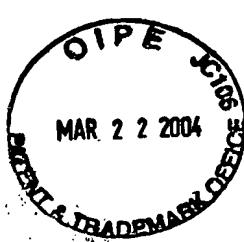
GATGAGTGTACGTGTCAGCTGCTGCCAGGCTTCAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTGGAGCAAGTTGCAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 110



AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGTGGAGGCAAGGAGGTCAAGGCAGCATCGGAAGCCAGGCCCTGGTACGTCAGACTCCCTCATCCCCAACCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGTCTCACCTCGAGGGTAAGGCAGTGTCACTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GCGGGCGCGGCCGCCCCGGCTCTGGCGCCCTGTGCTGGACGATATCCACAGGGCTGGCAGCCTCGTGTGCTGTGCGGGCCAGGACCCGCGCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGGTGCCTGGTATGCCGTGGTCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCCGCCATGGCACGTCGCAAGGCCCTCAAGAGGCCACGTCACCTTGACAGACCTCCAGCCGATCGCACAGTTCGTGGCTCACCTGCAGGAGACCAGCCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCCGTCGTATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACCTCATGTCACCGCCATCGCACAGCCGCTGCATAGGGCAAGTCCAGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCGAGGCCATCCTCTCCACGCTGCTGAGCTGACAGGAGAACAGCTGTTGGGGATTGGGGACGGCTGCTCTGCTTGGTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D
TGATTTCTTGTGGTACACCTCACCTCACCCAGCGAAACCTCTCAGGACCTGGTCCGAGGTGCTCTGAGTATGGCTGCGTGGTAACCTGGGAAGAACAGTGGTAACTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGTAGAAGACGAGGCCCTGGTGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGCCTGCTGCTGGATACCCGACCCCTGGAGGTGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S
CTATGCCGGACCTCATCAGAGCCAGTCACCTCAACGCCGCTCAAGGCTGGAGGAACATGGCTGCAACTCTGGTCTGCTGGTAAGTGTACAGCCTGTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D
TTGCAGGTAAACAGCTCCAGCGTGTGACCAACATCTACAAGATCCTCTGCTGAGGCTACAGGTTACGCATGTCGTGAGCTCCATTATCAGCAAGTTGGAAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N
CCCCACATTTCTGCGCTCATCTGACACGCCCTCCCTGCTACTCCATCCTGAAAGCCAAGACGCAAGGGATGTCGTGGGGCAAGGGCGCCGCCCTGCGCTCCGA
P T F F L R V I S O T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E
GGCGTGCAGTGGCTGTGCAACAGCTTCAGGCTGACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTACCTACGTCACCTGGTCACTCAGGACAGCCAGCGAGCTGGAAAGCTCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A O T Q L S R K L P
GGGGACGACGCTGACTGCCCTGGAGGCCAGCCAACCCGGCACTGCCCTGAGACTTCAGAACGATCCTGGACTGATGGCACCCGCCAGGCCAGAGCAGACACCAGGCC
G T T L T A L E A A A N P A L P S D F K T I L D
CTGTACGCCGGCTCATGCTCCAGGGAGGGGGGGCCACACCCAGGCCAGCCGCTGGAGTGTGAGCTGAGTGTGTTGGCCAGGCCCTGCATGTCGGCTGAAGGCT
GAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGTGAAGTGTCCAGCACCTGCCCTTCATTCGGCTCACAGGCTGGCCTGGCTCCACCCAGGGCAGCTTCTCAC
CAGGAGCCCGCTTCACTCCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTCACCCCTGCCCTGCCCTTGCCTTCCACCCCAACCATCCAGGTGGAGACCCCTGAGAA

Fig. 11P



GGACCCCTGGGAGCTGGGAATTGGAGTGACCAAGGTGTGCCCTGACACAGGCAGGACCTGCACCTGGATGGGGTCCCTGTTGAAATTGGGGGAGGTGCTGGAGTAA
AATACTGAATATGAGTTTCAGTTGA

Fig. 11Q



Truncated protein that lacks motif A

ATGCCGCGCGCTCCCCGCTGCCAGGCCGTGCCCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCGCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGCTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGCCCTGGGACGCACGGCCGCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCCTCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGCGAGCGCGCGCGAAGAACGTGCTGCCCTGGCCTGCCCTGCTGGACGGGGCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTTACCAACCAGCGTGCAGCTACCTGCCAACACGGTACCGGACCCACTGCCGGGAGCGGGGCGTGGGGCTGCTGCCTGCCGCTGGCGACGAGCT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D O V

GCTGGTTCACCTGCTGGCACGCTGCGCCTTTGCTGGTGGCTCCAGCTGCCCTACAGGTGCTGGGCCCTGCTACCAGCTGGCGCTGCCACTCAGGCCGGCCCG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGGGACCCGAAGGGCTGGGATCGAACGGCGCTGGGACCGTGGGACCCCTGGGCTGGGCCCTGGGCTGGGCCAGGCCGGGTGCCAGGCCGGGTGCCAGGCCGG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTGCCAACAGGGCCAGGCCTGGCGCTGCCCTGAGCCGGAGCGACGCCCTGGGCTGGGCCACCCGGCAGGACCGTGGACCGAGT
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTTGCTGGTGTACCTGCCAGACCCGCCAACAGGCCACTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGGGCCAACACGCCGGGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGCTCCCTGGGACACGCCCTGCCCCGGTACGCCAGACCAAGCACTCCCTACTCCTCAGCGACAAGGAGCAGCTGCCCTCCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTCTGAGGCCAGCTGACTGGCGTCGGAGGCTGTGGAGACCATCTTCTGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCGCTGCCAGCGCTACTGCCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCACGCCAGTGCCCTACGGGGTGTCTCAAGACGCACTGCCCGTGCAGCTGCCACCCAGCAGGCCGTCTGTGCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGGCCAGGGCTCTGGCGGCCCGAGGGAGGACACAGACCCCGTGCCTGGTGAGCTGCCAGCACAGCAGGCCCTGGCAGGTGACGGCTCGTGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R O H S S P W Q V Y G F V R A C

CCTGCGCCGCTGGTGCCTGCCAGGCCCTGGGCTCCAGGCACACGAAACGCCGCTCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGGCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCGTGCAGGAGATCTGGCCAAGTTCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGTCAGCTGCTAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAGAACAGGGCTTTTACCGGAAGAGTGTGGAGCAAGTTGCAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11R



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCAGGGAGCTGTCGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTCGGCCGATTGTGAACATGGACTACGTCGTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCCGTCTCACCTCGAGGGTGAAGGCACTGTTAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GCGGGCCGCCGCGCCCGCCCTCTGGGCCCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGACCTCTGTGCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCTCGGTATGCCGTGGTCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCCGCCATGGCACGTCGCAGGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCGACAGTTCTGGCTACCTGCAGGAAGACAGCCCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCCGTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCCTTCGACGTTCTACGCTTATGTGCCACACGCCGTGCGCATCAGGGCAAGTCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGGATCCCGAGGGCTCATCTCTCCACGCTGCTGCAAGCTGTGCTACGGGACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCGTTGGTGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L R L V D
TGATTTCTTGTGGTACACCTCACCTCACCGCGAAACCTCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGCGGAAGACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGTAGAACGAGGCCCTGGTGGCACGGCTTGTCAAGATGCCGCCACGGCTATTCCCTGGTGGCGCTGCTGGATAACCCGACCCCTGGAGGTGAGAGCAGACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R
GTGACCGCACCTGGCCGAAGTGGAGCCGTGCCCCGCTGGCCAGGTGCTGCTGAGGGCGTTGGCTCCACCTCTGCTTCCGTGCCCCAGGGACTGCCAATCCAAAGGGTCAGA
*
TGCCACAGGGTCCCCCTGTCCATCTGGGCTGAGCACAAATGCATTTCTGTGGAGTGAGGTGCTCACACGGAGCAGTTCTGTCTATTTGGTAA.....

Fig. 11S



Lacks motif A and altered C-terminus

ATGCCGCGCCTCCCGCTGCCGAGCCGTGCCCTCCCTGCTGCCAGCCACTACCGGAGGTGCTGCCGCTGCCACGTC
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCTTCCGCGCTGGTGGCCAGTGCCCTGGTGTGCCCTGGGACGCA
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCCAGTGCTGCCAGAGGCTGTGCCAGGCGCCGAAGAACGCTGCCCTGGCT
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCCTCACCAACCGTGCAGCTACCTGCCAACCGTACCGTACCGACTGCCGGGAGCGGGCGTGGGCTGCTGCC
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACGCTGCCCTTGTGCTGGCTCCAGCTGCCCTACAGGTGCTGCCAGCTGCCACTCAGGCTGCCACT
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGGGACCCGAAGGCGTGGGATCGAACGGGCTGGGACCCATAGCGTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGGCCGG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTGTGCCGTGCCAGAGGCCAGGCCTGGCGCTGCCCTGAGCGAGCGACGCCCTGGCAGGGCTGGGCCACCCGGCAGGAC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTTGCTCACCTGCCAGACCCCGAAGAACCCACTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGGCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACCGCCCTGGACACGCCCTGTCGGGGACCGCTGGGGGGTACCCGAGACCAAGCAGCTCCCTACTCC
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTCTGAGGCCAGCCCTGACTGGCGCTGGAGGCTGTGGAGACCATCTTCTGGGGTCCAGGCCGGATGCCAGGGACT
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W O

AATGCGGCCCTGTTCTGGAGCTGCTGGGAACACGCGCAGTGCCCTACGGGGTGCTCAAGACGCACTGCCGCTGCAG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGGCCAGGGCTGTGGCGGCCAGGGACACAGACCCCGTCCGGTGCAGCTGCCAGCACAGCAGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R O H S S P W Q V Y G F V R A C

CCTGCCGCCGCTGGTCCCCAGGCCCTGGGGCTCCAGGACA
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGGACTGGCTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGGCCAGAGC
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W I

GATGAGTGTGACGTGAGCTGCTAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCT
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T



AATCAGACAGCACTGAAGAGGGTGCAGCTGGGGAGCTGTCGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCCCCTGCTGACCTCCAGACTCCGTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGGGCCATTGTGAACATGGACTACGTGTTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGTCTCACCTCGAGGGTAAGGCACTGTTAGGGTGTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCCCGGCTCTGGCGCCTCTGTGCTGGGCTGGACGATATCACAGGGCTGGCCACCTCGTGTGCGTGCGGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGCAAG GACAGGCTACGGAGGTACGCCAGCATCAAAACCCAGAACACGTACTGCGTGCCTGGTACCTGCAGGGACCCGCTGAGCTGCGTGCCTGGTACCTGCAGG
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGCACGTCGAAGGCCACGCTCTACCTGACAGACCTCCAGGGTACATGCCACAGTTCGAGCTGGCTCACCTGCAGGGACCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TCCGCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTCACGCTCATGTGCCACCCAGGGCGCATCAGGGCAAGTCACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCATCTCCACGCTGCTGAGCCAGATGGAGAACAGCTGTTGGGGATTGGCGGGACGGCTGCTCTGCCTGGTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTCTTGGTGAACCTCACCCACGGCAAACCTTCTCAGGACCTGGTCCAGGAGGTGCTGAGTATGGCTGCTGGTAACCTGGAAAGACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGTGGCACGGCTTGTCAAGATGCCGCCACGGCTATTCCCTGGTGGCGCTGCTGGATAACCGGACCCGGAGGTGAGACGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCGGACCTCCATCAGAGCCAGTCACCTCAACCGCCGCTCAAGGCTGGAGGAACATGCCGAAACTCTTGGGCTTGGCTGAAGTGTACAGCTGTTGG
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F D

TTGCAGGTGAACAGCCTCAGACGGTGTGACCAACATCTACAAGATCCTCTGCAAGGCTACAGGTTACGCATGTGCTGCAGCTCCATTCA
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTCTGCGCGTCACTCTGACACGGCCCTCTGTAACCTGAAAGCCAAGAACGCAAGGGATGCGTGGGGCAAGGGGCCGCGCCCTGCCCCTGA
P T F F L R V I S O T A S L C Y S I L K A K N A E

CCGAAGAAAACATTCTGCTGACTCCTGGCTGCTGGTC
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGACCCACCCGAGACCGTGGGTGAGCTTCCGGTGTCTGGAGGGAGTTGGCTGGCTGTGACTCCTCAGCCTGTTCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *



Truncated telomerase (ver. 2)

ATGCCGCGCCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCGCTGCCACGTCGT
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCCTGGTGTGCCTGGCCTGGGACGCACGGCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GCCCTCCCCGGGTGGCGTCCGGCTGGGTTGAGGGGGCCGGGGAAACAGCGACATGCGGAGAGCAGCGCAGGCACTCAGGGCGCTCCCCGCGGT
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCCCGCCAGGTGTCCTGCCCTGAAGGAGCTGGTGGCCAGTGCTCCAGAGGCTGTGCAGGGCGCGGAAGAACGTGCTGGCCTTCGCCCTGCCCTGCCCTGGACGGGGCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTTACCAACCGCGCAGCTACCTGCCAACACGGTACCGACGCAGTGGGGGAGGGGGCTGCTGCCCTGCCCTGGGACGAGCT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACGCTGCCGCTTTGTGCTGGTGGCTCCAGCTGCCCTACAGGTGTGCGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGGCCGGCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCCTGGATGCGAACGGCTGGAACCATAGCGTAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCCGGTGCAGGAGGCCGGAGCT
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTGCCAACAGGCCAGGCCTGGCGCTGCCCTGAGCCGAGCCGACGCCCTGGCAGGGCTGGGCCACCCGGCAGGACCCGTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTTGCTGGTGTACCTGCCAGACCCGCCAGAAGGCCACCTTTGGAGGGTGCCTCTGGCACGGCCACTCCACCCATCCGTGGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCACACGCCCTGGACACGCCCTGGTACGCCAGACCAAGCAAGCACTCCCTACTCCCTAGCGACAAGGAGCAGCTGCCCTCCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTGTGGAGACCATTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGGCCCTGCCAGCGCTACTGCCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACCCAGCGCAGTGGCCCTACGGGTGCTCTCAAGACGCAGTGGCGCTGCCAGCTGGTACGGCTGCCAGCGCAGGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGGCGCCCGAGGAGGAGCACAGACCCCGTCCCTGGTCAGCTGCCAGCACAGCAGGCCCTGGCAGGTGACGGCTCTGCCAGGGCT
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTGCCTGCCAGGCCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACCCAAGAAGTCATCCCTGGGAAGCATGCCAGCTCGCTGCCAGGGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11V



GACGTGGAAGATGAGCGTGCAGGACTGGCTGGCTGGCAGAGCCCAGGGTTGGCTGTTCCGGCCCCAGAGCACCGTCTGGCTGAGGAGATCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L
GATGAGTGTGACGTGCTGAGCTGCTCAGGCTTTCTTTATGTCACGGAGACCGACGTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
AAT--NNN--GACAGTCACCAGGGGGTTGACCGCCGACTGGCGTCCCCAGGGTTGACTATAGGACCAAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTAGAGGCCTGGCTGG
CATGGGTGGACGTGGCCCCGGCATGGCTTCTGCGTGTGCTGCCGTGGGTGCCCTGACCTGAGTCGGTGGGGCTGTGGCTCCGTGAGCTTCCCCTAGTCAGCTGTTGCTG
GCTGAGCAAGCCTCTGAGGGCTCTATTG..

Fig. 11W



Truncated protein 1 (ver. 2)

ATGCCGCGCGTCCCCGCTGCCAGCCGTGCCTCCCTGCTGCAGGCCACTACCCGAGGTGCTGCCCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCTGGTGTGCCCTGGGACGACGGCCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCGGGTGGCGTCCGGCTGGGTTGAGGGCGCCGGGGAACAGCGACATGCCAGAGCAGGCCACTCAGGGCTTCCCCCAGGT
G L P G V G V R L G L R A A G G N O R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCCCGCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCTGCAGAGGTGCTGCCAGGCCGCGGAAGAACGTGCTGGCTTCCGCTGCTGGACGGGGCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGACGCACTGCCGGGGAGCGGGCGTGGGGCTGCTGCCGCGTGGCGACGG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCCGCTTTGTGCTGGTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGGCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTGGATGCAACGGCTGGAACCATAGCGTCAGGGAGGCCGGTCCCGCTGGCTGCCAGCCGGGTGCGAGGAGGCCGGGGAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGCTGCCAGGCCAAGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAAGAAGCCACCTTTGGAGGGTGCCTCTCTGGCACGCCACTCCACCCATCCGTGGCCGCCAGCACGCCGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCACCAAGCTCCCTGGACACGCCCTGGTACGCCAGAGCAAGCACTCCCTACTCCTCACGGCACAAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTCTGAGGCCAGCTGACTGGCGCTCGGAGGCTGGAGAACATCTTCTGGTCCAGGCCCTGGACTCCCGCAGGTGCCCCGCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTCCCCACTGGGGTCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGGCCAGGCCAGGCCAG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGGAGGGACACAGACCCCGTCGCTGGAGCTGCCAGCTGCCAGCACAGCAGGCCCTGGCAGGTGACGGCTCGC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCAGGCCCTGGGCTCCAGGACAACGACGCCCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S I Q E L

Fig. 11X



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTTGGCTGCGCAGGGAGCCAGGGGTTGGCTGTGTTCCGGCGCAGAGCACCGTCTGCGTGAAGAGATCCTGGCCAAGTTCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTAACGTGTCGAGCTGCTCAGGTCTTCTTTATGTACCGGAGACCACTTCAAAAGAACAGGTCTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCCGGAGCTGTCGGAAGCAGAGGTAGGCAGCATCGGGAAAGCCAGGCCCGCCCTGCTGACGCCAGACTCCGCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTGGTTAACCTCCCTTTAACAGAA
V A V L W F T F L F N Q K

CGGGCTGCCGCGATTGTGAACATGGACTACGTCGTGGAGGCCAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G *

Fig. 11Y



Truncated protein 2 (ver. 2)

ATGCCGCGCCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGCTCGCTGAGGCTGGCCAGGCTGGCCACGCGACGCCGCCCCCGCGC
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCCTGGGCCCCAGGGCTGGCGCTGGTGAGCGCGGGACCCGGCGCTTCCCGCGCTGGTGGCCAGTGCTGGTGGCCAGTGCTGGTGGCCAGTGCTGGCCTGGGACGACGCCGCCCCCGCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGCGCGTCCGGCTGGGTTGAGGGCGCCGGGGAACCGCGACATGCCGAGAGCACCGCAGGCACTCAGGGCGCTTCCCCGAGGGT
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCCCTCCGCCAGGTGCTCTGCCAGAGGAGCTGGTGGCCGAGTGCTGCCAGGGCTGTGCCAGGCCGCGAGAACGTCGCTGGCCTTCGGCTCGCCTGCTGGACGGGCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCCTCACCAACAGCGCGCAGCTACCTGCCAACACGGTACCCGACGCACTCGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCGCGTGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACCTGCTGCCACGGCTGCCGCTCTTGCTGGCTCCAGCTGCCCTACCAAGGTGCTGCCAGGCTGCTGCCACTCGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCGCGTGGCGACGACGT
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACCCCTAGTGGACCCGAAGGGCTGGGATGCCAACGGGCTGGAACCATAGGGTCAAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCCCGGTCCGAGGAAGGGCGGGGAGGTGCA
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAACAGGGCCAGGGCTGGCCTGCCCTGACCCGGAGCGACGCCGTGGGAGGGCTCTGGGCCACCCGGCAGGACGCCGTGGACCCGACTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTTGCTCACCTGCCAGACCCGCCAGAGGCCACTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGGGGCCAGCAGCACGCCGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCCGCCACCAAGCTGGACACGCCCTGGACAGCCCTTGCTCCCCGGTGTACGCCAGAACCAAGCCTTCCTACTCCAGGCACAAAGGAGCAGCTGCCGCTCTTCCACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCTGACTGGCCTGGAGGGCTGGAGACCATCTTCTGGGCTGCCAGGGCTGGATGCCAGGGACTCCCGCAGGGTGGCCCTGCCAGGCCACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTGCCCTACGGGTGCTCAAGACCAAGCCTGCCGCTGGAGCTGCCACTGCCAGCAGGCCGTC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGGCGCCCCAGGGACAGAGACCCCGTGCCTGGTGAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGGCTCGCTGAGGCT
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CTGCGCCGGCTGGTGGCCCAAGGCTCTGGGCTCCAGGCACACGAGCCGCTCCAGGAACACCAAGAAGTCATCTCCGGAAAGCATGCCAAGCTCGCTGCCAGGACT
L R R L V P P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11Z



GACGTGGAAGATGAGCGTGGGGACTGCGCTGGCTGCGCAGGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGTCTGCGTGGAGATCCTGGCCAAGTTCTGCACGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGCTGAGCTGCTCAGGTTCTTATGTCACGGAGACCGACGTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGCGGAAGCAGAGGTAGGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTCATCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGCCGATTGTGAACATGGACTACGTCGTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGACTGTTCAAGCTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGCCGCGCCGCCCCGGCTCTGGCGCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGGCACCTTCGTGCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCCGTACGACACCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACAGTACTGCGTGCCTGCGTATGCCGTGGTCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGCACGTCGCAAGGCCCTCAAGAGCCAC
K A A H G H V R K A F K S H

GTCTACGTCCAGTG
V L R P V

CCAGGGGATCCCGCAGGGCTCATCCCTCCACGGCTGCTCTGCACCCCTGTGCTACGGGACATGGAGAACAGCTGTTGGGGGATTCGGGGGACGGCTGCTCTGCCTTGGTGA
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G

TGATTCTTGTGGTACACCTCACCTACCCACGGAAAACCTCCTCAGGACCCGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGGGAAGAACAGTGGTAACCTCCC
*

Fig. 11AA



Reference protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGCAGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGGCTTCCGCGCCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCCCGCCGCCCTCCTCCGCCAGGTG	
AspAlaArgProProProAlaAlaProSerPheArgGlnVal	
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAG	
G L P G V .G V R L G L R A A G G G N Q R H A E	
A S P G S A S G W G * G R P G G T S D M R R	
P P R G R R P A G V E G G R G E P A T C G E	
AGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG	
S S A G D S G R F P R R	
A A Q A T Q G A S P A G	
Q R R R L R A L P P Q V	
TCCTGCCTGAAGGAGCTG	240
SerCysLeuLysGluLeu	80
GTGGCCCAGTGCTGCAGAGGCTGTGCGAGCGCGGCCGCGAAGAACGTGCTGGCCTCGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGGACGGGCCGCGGGGGCCCCCGAGGCCTTCACACCAGCGTGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCCTGCGGGGGAGCGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCAGCTGCGCTACCAGGTGTGCGGGCCGCCGCTGTACAGCTGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200

Fig. 11AB



CGCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCCTGCCAGCCCCGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGTCTGGGCCACCCGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTTTGGAGGGTGCCTCTCTGGCACGCCACTCCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACACGCCGGCCCCCATCCACATGCCGCCACACGTCCCTGGCACGCC	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCGGTGTACGCCGAGACCAAGCACTTCCCTACTCCTCAGGCAGAACGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTCGGTACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCAGTGCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTCGGTACCAC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGCCCCGGAGAACGCCAGGGCTCTGGCGGCCGGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGTCGCTGGTGAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTCGTGCAGGAGCTGACGTGGAAAGATGAGCGTGCAGGGCTGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGGAAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
GCCAAAGCTCTCGCTGCAGGAGCTGACGTGGAAAGATGAGCGTGCAGGGCTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520

Fig. 11AC

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CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
TTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTC PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	1740 580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTCGGAAGCAGAGGTCAAGCAGCATCGGGAAAGCCAGGCCGCCCTGCTGACGTCCAGA LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	1860 620
CTCCGCTTCATCCCCAACGCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
GGAGGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCA GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	1980 660
CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCTCGCTGGCGCCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	2040 680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGCCTGGCGCCTGTG LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	2100 700
GACCCGCCCTGAGCTGTACTTGCAAGGTGGATGTGACGGCGCGTACGACACCATC AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGC ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	2220 740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCATGGCACGTCCGCAAGGCCTCAAG ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	2280 760
AGCCACGTCTTACCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCTCTCGACGTCTCGCTACGCTTCAATGTGCCACCACGCCGTGCGCATT AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840

Fig. 11AD



CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCGGGGATTGGCGGGAC	2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
GGGCTGCTCCTGCGTTGGATGATTCTTGGTACACCTCACCTCACCCACGCG	2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGTGGCACGGCTTTGTT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCCACGGCCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGGACCCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCACCTTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AACCGCGGCTTCAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGGCGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCCTGTTCTGGATTGAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGCTGCAGCTCCCA	3060
IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTGGAAGAACCCACATTTCCTGCGCGTCATCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

Fig. 11AE



Truncated protein 3 (ver. 2)

Fig. 11AF



GACGTGGAAGATGAGCTGGGGACTGCCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTTCCGGCGCAGAGCACCGTCTGCGTGGAGAGATCCTGGCCAAGTTCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTCTTTATGTCACGGAGACCACTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACACCACTTGAAGAGGGTGAGCTGCCAGAGGTAGGCAGCATGGGAAGCCAGGCCCTGCTGACGTCAGACTCCGTTATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCCGCGATTGTGAACATGGACTACGTGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGTCTACCTGAGGGTAAGGCAGTTCAGGTGCTCAACTAGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGCCGCGGCCCGCCCTCTGGCGCCTGTGCTGGCCTGGACGATATCCACAGGGCTGGGCACCTCGTGTGCGTGTGCGGCCAGGACCCCGCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGCGCTACGACACCATCCCCAGGACAGGCTACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGCACGTCGCAAGGCCCTCAAGAGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCGACAGTCGTCGCTCACCTGCA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTCAGCTCTACGCTCATGTGCCACACGCCGCGCATCAGGGCAAGTCTACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V O C

CCAGGGGATCCGCAGGGCTCATCTCCACCGCTCTGCAGCCTGTGCTACGGGACATGGAGAACAGCTGTTGGGATTGGCGGACGGCTGCTCTGGTTGGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTACACCTCACCTACCCACGCAGAACCTTCCTCAGGACCTGGTCCAGGCTGAGTATGGCTGCGTGGTAACCTGGGAAGAACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGAGAACGAGGCCCTGGTGGCACGGCTTGTGAGATGCCGCCACGGCTATTCCCTGGTGGCTGCTGGATAACCCGACCTGGAGGTGAGAGCAGACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

TGAGGCCACCTGGCCGAAGTGGAGCCCTGCCCCGCTGGGAGGTGCTGCAAGGGCTTGGTCCACCTCTGTTCCGTGTGGGAGGGCACTGCCAATCCAAAGGGTCA
*

TGCCACAGGGTCCCCCTGTCATCTGGGCTGAGCACAAATGCACTTCTGAGGTGCTCACACGGAGGAGTGGTCTGCTGCTGCTGCTATTTGGTAA...

Fig. 11AG



Altered C-terminus protein (ver. 2)

Fig. 11AH



GACGTGGAAGATGAGCGTGGGGACTCGCCTGGCTGCGCAGGGAGCCAGGGGTGGCTGTGTTCCGGCGAGAGCACCGTCTCGCTGAGGAGATCTGGCAAGTTCTGACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGTCAGCTGCTCAGGCTTTATGTACGGAGACACGTTCAAAGAACAGGCTTTCTACCGAAGAGTGTCTGGAGCAAGTGCCTGAGGAGATGGCT
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGCGAAGCAGGGTCAGGAGCATCGGAAGCCAGGCCGCGCTGCTGACGTCCAGACTCCGCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGCTCACCTGAGGGTAAGGCAGTGTCACTACAGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGCCCTCTGGCGCTCTGTCTGGCTGGACGATATCCACAGGGCTGGCCACCTCGCTGCTGCGTGTGCGGCCAGGACCCGCGCTGAGGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGCGCGTACGACACCATCCCCAGGGACAGGCTACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTACTCGCTGCTGGTATGCCGTGGTCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCCATGGCACGTCGCAAGGCCCTCAAGAGCACGTCACCTTGACAGACCTCCAGCGTACATGCGACAGTCGCTGGCTCACCTGAGGAGACCCGCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTCCACGCTCATGTGCCACACGCCGTGCGCATCAGGGCAAGTCCTACCTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCGCAGGGCTCCATCTCTCACCGCTGCTGAGCGCATGGAGAACAGCTGTTGCCGGGATTGGCGGGACGGGCTGCTCTGCCGTGGTGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTACACCTCACCTCACCCACGCCGAAACCTCTCAGGACCTGGTCCAGGAGGTGTCCCTGAGTATGGCTGCGTGGTGA
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAACGAGGCCCTGGGTGGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGACCCCTGGAGGTGCAGAGCAGACTCCG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCGGACCTCCATCAGAGCCAGTCACCTCACCGCCGCTCAAGGCTGGAGGAACATGCGTCGAAACTCTTGGGTCTGCGCTGAAGTGTACAGCCTGTTCTGG
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTGCAGGTGAACAGCCTCAGACGGTGTGCAACCAACATCACAAGATCCTCGCTGCAAGGCTACAGGTTCACCGATGTGCTGAGCTCCATTCTACAGCAAGTTGGAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTCTCCGGTCTGACACGGCTCCCTCTGCTACTCCATCTGAAAGCAAGAACGAGGGATGCGCTGGGGCCAAGGGCCGCCCTGCCCCCTGCCCC
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTCTGCTGACTCTGCGGTGCTGGTC
E E N I L V V T P A V L G S

GGGACACCCAGAGATGGAGCCACCCCGAGACCGTCGGTGGGCAGTTCCGGTGTCTCTGGAGGGAGTTGGCTGGGCTGTGACTCTCAGCTCTGTTCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11AI



Protein that lacks motif A (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCACCTCGT
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCCGCCCTGGGGCCCAGGGCTGGCGCTGGTGCAGCCGGGGACCCGGCGCTTCCGGCGCTGGTGGCCCA
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCCTCCCGGGGTGGCGTCCGGCTGGGTTGAGGGCGCCGGGGAAACAGCAGCAGATGCGAGAGCAGCG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCAGAGCTGTGCAGCGCGCGAAGAAC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGGCCCCCGAGGCTTACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCAGCAGCTGGGG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCCTTGTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGGCTAGGGACCCGAAGGGCTGGATGCGAACGGCTGGAACCATAGCGTCAGGGAGGCCGG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTGTGCCGTGCCAGAGGGCCAGGCAGCCGGCTGCCCTGAGCCGGAGCGGACGCC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTTGTCACCTGCCAGACCCGCCAGAGGCCACCTCTTGGAGGGTGCCTCTGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGTCCCTGGACACGCCCTGGTACGCCAGACCAAGC
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTCTGAGGCCAGCCTGACTGGCCTGGAGGCTGTGGAGACCATTTCTGG
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCAACGCCAGTGCCCTACGG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGGGGCCCCAGGGAGGGACACAGACCC
E K P Q G S V A A P E E E D T O P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCTCCAGGCACA
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AJ



ACCTGGAAAGTGGCGGGACTGGCTGGCAGGAGCCCAGGGTGGCTGTTCCGCCAGAGCACCGTCTGGTGGAGAGATCTGGCAAGTCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGAGCTGAGCTGAGCTTATGTCAGGCTTCTTCTACGGAGACACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGCGGAAGCAGAGGTAGGCAGCATCGGGAGCCAGGCCGCCCCTGCTGACGTCCAGACTCCCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCCGCCATTGTGAACATGGACTACCTCGTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCACTCTGAGGGTAAGGCACTGTTAGCGTCTCAACTACGA
G L R P I V N M D Y V V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

CGGGGCCGCCGCCGCCCTCTGGGCCCTCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGCACCTCGTGTGCTGTGCGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGATGCCGTTGCGTCAACTACGA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAAGCCGCCATGGCACGTCGCAGGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCCACAGGGCTGCCATCAGGGCAAGTCTACGCCAGTG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGCTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTCTACGCTCATGTGCCACACGCCGTGCCATCAGGGCAAGTCTACGCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGCAGCCTGTGCTACGGGACATGGAGAACAGCTGTTGCGGGATTCCGGGACGGCTGCTCTGCGTTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTACACCTCACCTCACCGAAAACCTCTCAGGACCTGGTGGAGGTGCTCTGAGTATGGCTGCGTGAACCTGCGGAAGAACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGTGGCACGGCTTGTCAAGATGCCGCCACGGCTATTCCCTGGTGGCTGCTGGATAACCCGACCTGGAGGTGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S O Y S S

CTATGCCGGACCTCATCAGAGCCAGTCACTTCAACCGGGCTCAAGGCTGGAGGAACATGCGTCGAAACTCTTGGGTCTGCGCTGAAGTGTCAAGCCTGTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTCAGGTGAACGCCAGACGGTGTGACCAACATCTACAAGATCTCTGCTGAGGCTACAGTTACGCAATGTGCTGCAGCTCCATTCACTAGCAAGTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTCTGGCGTCATCTGACAGGCCCTCTGCTACTCCATCTGAAAGCCAAGAACGCCAGGGATGCGCTGGGGCAAGGGGCCGCCCTGCGCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGAGTGGCTGTGACCAAGCATTCTGCTCAAGCTGACTGACACCGTGTACCTACGTCACCTGGGTACTCAGGACAGCCAGACGCACTGAGTCGGAAGCTCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGAGCTGACTGCCCTGGAGGCCAGCCAACCCGCACTGCCCTCAGACTCAAGACCATCTGGACTGATGCCACCCGCCACAGCCAGGCCAGAGCAGACACCAGCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D

Fig. 11AK



CTGTACGCCGGCTCACGTCCAGGGAGGGGGCGGCCACACCCAGGCCGACCGCTGGAGTCTGAGGCTTGAGTGAGTGTGTTGCCGAGGCCTGCATGTCGGCTGAAGGC
GAGTGTCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCAGCACACCTGCCGTCTCACTTCCCCACAGGCTGGCGCTGGCTCCACCCCCAGGGCCAGCTTCTCAC
CAGGAGCCCGCTTCACTCCCCACATAGGAATAGTCCATCCCAGATTGCCATTGTTACCCCTGCCCTGCCCTCTTGCTTCCACCCCCACATCCAGGTGGAGACCCCTGAGAA
GGACCCCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGACACAGGCAGGACCCCTGACCTGGATGGGGTCCCTGTGGTCAAATTGGGGAGGTGCTGGAGTAA
AATACTGAATATGAGTTTCAGTTGA

Fig. 11AL



Truncated protein that lacks motif A (ver. 2)

ATGCCGGCGCTCCCGCTGCCAGCCGTGGCTCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCCTGGCCACGTTGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCCTGGGGCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCCTGGTGTGCCTGGCCACGCA
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGGCGCTGGGTGAGGCCGGGGAAACAGCAGACATGCCAGAGCAGCGCAGGCACCTGGCGCTTCCCCGAGGTG
G L P G V G V R L G L R A A G G N O R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGCTGCGAGCGGGCGCGAAGAACGTCGGCTCGCTGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCCCGAGGCCTTACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCAGCAGTGGGGAGGGCGTGGGGCTGCTGC
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACCTGCTGGCACGCTGCCTTGTGCTGGCTCCAGCTGCCAACAGGTGCGGGCGCCGCTGTACAGCTGGCGCTGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCGTCTGGATGCGAACGGCCTGGAACCATAGCGTACGGAGGCCGGTCCCCCTGGCCTGCC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGCCAGCGCTGGCGCTGCCAACCTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCC
S R S L P L P K R P R R G A A P E P E R T P V G O G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGCCGGCGAAGAAGCCACCTCTTGAGGGTGCCTCTGGCACGCCACTCCACCCATCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACCGCTGGACACGCCCTGGTACGCCAGAACGACTTCTACTCTCAGCGACAAGGAGCAGCTGG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGGGCCAGCCTGACTGGCGCTGGAGGGCTGTGGAGACCATTTCTGGTCCAGGCCCTGGATGCCAGGACTCCCC
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGGGGCCCTGTTCTGGAGCTGCTGGGAACCAACGCCAGTGCCACTGGGTGCTCTCAAGACGCACTGCCGCTGCCAG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGGCGGCCAGGGAGAGACAGACCCCGTGCCTGGTCAAGCAGCAGCCCTGGCAGGTGACGG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CTGCGCCGGCTGTGCCCCAGGCCCTGGGGCTCCAGGCACAACGAACGCCGCTCTCAGGAACACCAAGAAGTCATCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AM



GACGTGGAAGATGAGCGTGGGGACTCGCCTGGCTGCGCAGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGTCTCGTGAGGAGATCCTGGCAAGTCTGACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGAGCTGCTCAGGTCTTCTTTATGTACGGAGACACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F O K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTGAAGAGGGTGCAGCTGGGAGCTGCGAAGCAGAGTCAGGAGCATGGAGCCAGGCCCTGCTGACGTCCAGACTCCGTTATCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGGCCATTGTGAACATGGACTACGTCGTTGGAGCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGCTCACCTGAGGGTAAGGACTGTCAGGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GGGGCGGGGCCCTGGGCCCTCTGGGCCCTGTGCTGGGCTGGACGATATCCACAGGGCTGGGCACCTCGTGTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGTGCGTATGCCGTGCTCAACTACGA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCCATGGCACGTCGCAAGGCCCTCAAGAGCCACGTCTACCTGACAGACCTCCAGCGTACATGCCACAGTCTGGCTCACCTGAGGAGACCAGCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGCTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTTCCACGCTTCCAGCTTCCACGCTTCACTGCGCACCACGCCGTGCGCATCAGGGCAAGTCTACCTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTCTGCAGGCTGTGCTACGGCAGATGGAGAACAGCTGTTGGGGATTCCGGGGACGGCTGCTCTGGTTGGTGA
Q G I P Q G S I L S T L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTCCTGTTGGTACACCTCACCTCACCGCAGAACCTCTCAGGACCCCTGGTCCAGGAGCTGCTGAGTATGGCTGGTGAATTGGAAAGACAGTGGTGAACCTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAACGAGGCCCTGGTGGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGACCTGGAGGTGAGACACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

TGAGGCCACCTGGCCGAAGTGGAGCCTGTGCCCCGTGGCAGGTGCTGCAAGGCCCTTCCGTCCACCTCTGCTTCCGTGGAGGCCACTGCCAATCCAAAGGGTCA
*

TGCCACAGGTGCCCTGTCATCTGGGCTGAGCACAAATGATTTCTGAGGTGCTCACACGGAGCAGTTCTGTGCTATTGGTAA

Fig. 11AN



Lacks motif A and altered C-terminus (ver. 2)

ATGCCGCGCTCCCGCTGCCAGCCGTGGCTCCCTGCTGCCAGCCACTACCGAGGTGCTGCCCTGGCACGTCG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGACGCACGGCCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCGGGTGGCGTCCGGCTGGGTTGAGGCCGGGGAAACAGCGACATGCGAGAGCAGCGAGGCAGTCAGGGCTTCCCCCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGCTGTGCGAGCGCCGCGGAAGAACGTGCTGGCTTCGGCTGCTGGACGGGCCCC
P S F R O V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGACGCACTGCCGGGAGCCGGCTGGGGCTGCTGCTGCCCGCGTGGCGACGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCCGCTCTTGTGCTGGCTCCAGCTGCCAACACGGTACCGACGCACTGCCGGGAGCCGGCTGGGGCTGCTGCTGCCACTCAGGCCGGCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGGCTAGTGGACCCGAAGGGCTGGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCGGGTGCAGGGAGGCCGGCAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGCGTGGCTGCCCTGAGCCGGAGCGACGCCCTGGCAGGGCTCTGGCCACCCGGCAGGACCGCTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTTGTCACCTGCCAACCCGCCAGAACGCAACTCTTGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGCTCCCTGGACACGCCCTGGTACGCCAGACCAAGCACTCTCTACTCCCTCAGGCACAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGGCTGTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCCTACTGGC
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGCCAGCAGCCGCTGCTGTGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGGCGGCCAGGGAGGAGGACACAGACCCCGTCGCTGGTGCAGCTGCTGCCAGCACAGCAGCCCTGCCAGGTGACGGCTCGTGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGCTGGGCCCTAGGCCCTGGGGCTCCAGGCACACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC
L R R L V P P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AO



GACGTGGAAGATGAGCCTGCGGGACTGCGCTGGCTGCGCAGGGAGCCAGGGGTTGGCTGTGTTCCGGCCAGAGCAGCGTCTGCGTGAAGGAGATCTGGCCAAGTTCTGACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGAGCTGCTCAGGCTTTATGTCACGGAGACACGTTCAAAGAACAGGCTTTCTACCGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGAGCTGCGGAAGCAGAGGTAGGCAGCATCGGAAGCCAGGCCGCGCTGCTGACGTCCAGACTCCGTTATCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGGCCATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGTCTACCTGAGGGTAAGGCACTGTCAGCGTCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GGGGCGGGGCCCTGGCGCTCTGGCGCCCTGTGCTGGGCTGGACGATATCCACAGGGCTGGGCACCTCGTGTGCGTGTGCGGCCAGGACCCGCCGCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTAACGTCGTCGTCGGTATGCCGGTCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCCCATGGCACGTCGCAAGGCCCTCAAGAGCCACGTCTACCTGACAGACCTCCAGCGTACATGCCACAGTCGTCACCTGCAAGGAGACCAGCCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGCTTCTACGCTCATGTCGACCGTGCATCAGGGCAAGTCCTACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGAGGGCTCATCCTCTCACGCTGCTGAGCCGACATGGAGAACAGCTGTTGGGGATTGGCGGGACGGCTGCTCTGCGTTGG
Q G I P Q G S I L S T L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTGAACCTCACCTCACCGCAAACCTTCTCAGGACCTGGTCCGAGGTGCTCTGAGTATGGCTGCGTGAACTGCGGAAGAACAGTGGTGAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGTGGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGGACCTGGAGGTGCAAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCGGACCTCATCAGAGCCAGTCACTTCAACCGGGCTCAAGGCTGGAGGAACATGCGTCGCAAACCTTGGGCTTGGCTGAGTGTCAAGCTGTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACGCCCTCACGGTGTGACCAACATCTACAAGATCTCTGCTGAGGTTCACGCTATGTCGTCAGCTCCATTCTACAGCAAGTTGGAGAA
I Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTCTGCGCGTATCTGACACGGCTCCCTGCTACTCCATCTGAAGCCAAGAACGCAAGGATGTCGCTGGGGCAAGGGCCGCCGCGCTGCGCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTCTGCGTGAACCTGGCTGCTGACTCCCTGCGCTGACTCCATTCTACAGCAAGTTGGAGAA
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGAGCTTCCGGTGTCTGGAGGGAGTTGGCTGGCGCTGACTCCTCAGCTCTGTTTCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11AP

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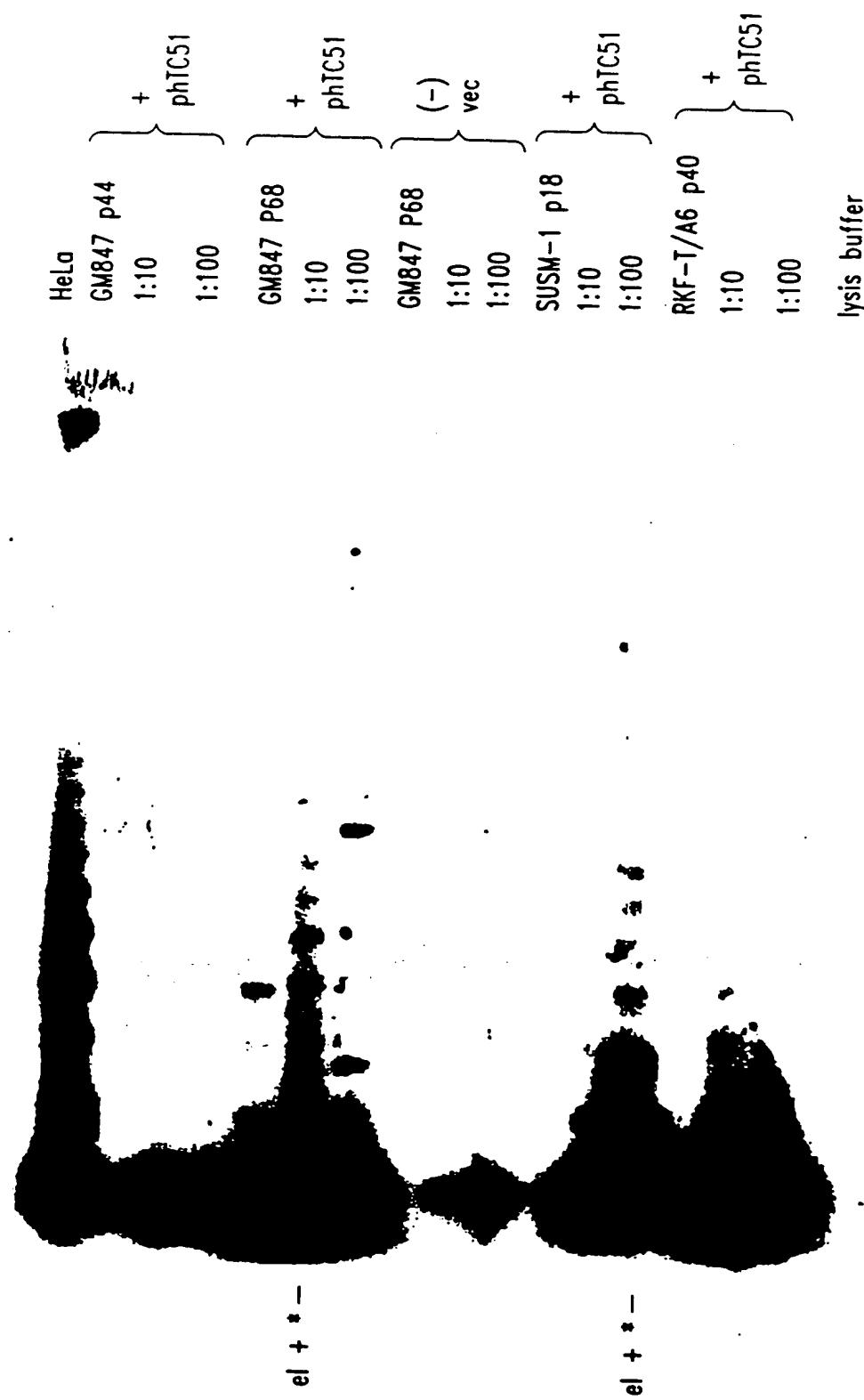


Fig. 12

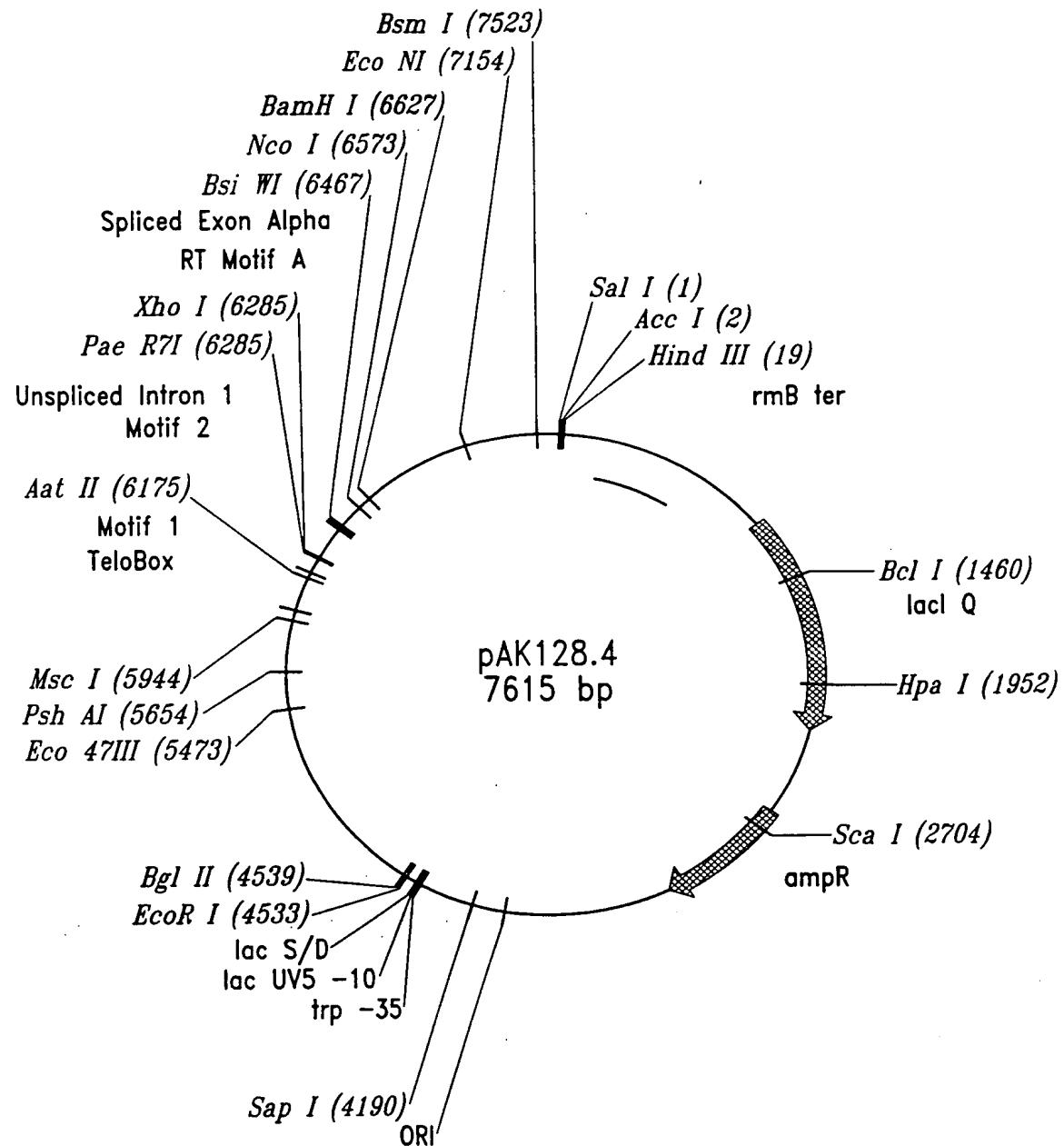


Fig. 13A



LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

Fig. 13B



Fig. 13C



5581 cagcagccgg tgtctgtgcc cgggagaagg cccaggggctc tgtggcgccc cccgaggagg
5641 aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg
5701 tgtacggctt cgtgcggggc tgccctgcgc ggctggtgcc cccaggccctc tggggctcca
5761 ggcacaacga acgcccgttc ctcaggaaca ccaagaagtt catctccctg gggaaagcatg
5821 ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc
5881 gcaggagccc agggggtggc tgtgtccgg cccagagca ccgtctgcgt gaggagatcc
5941 tggccaagtt cctgcactgg ctgatgagt tgtaacgtcgt cgagctgctc aggtcttct
6001 tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct
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Fig. 13D

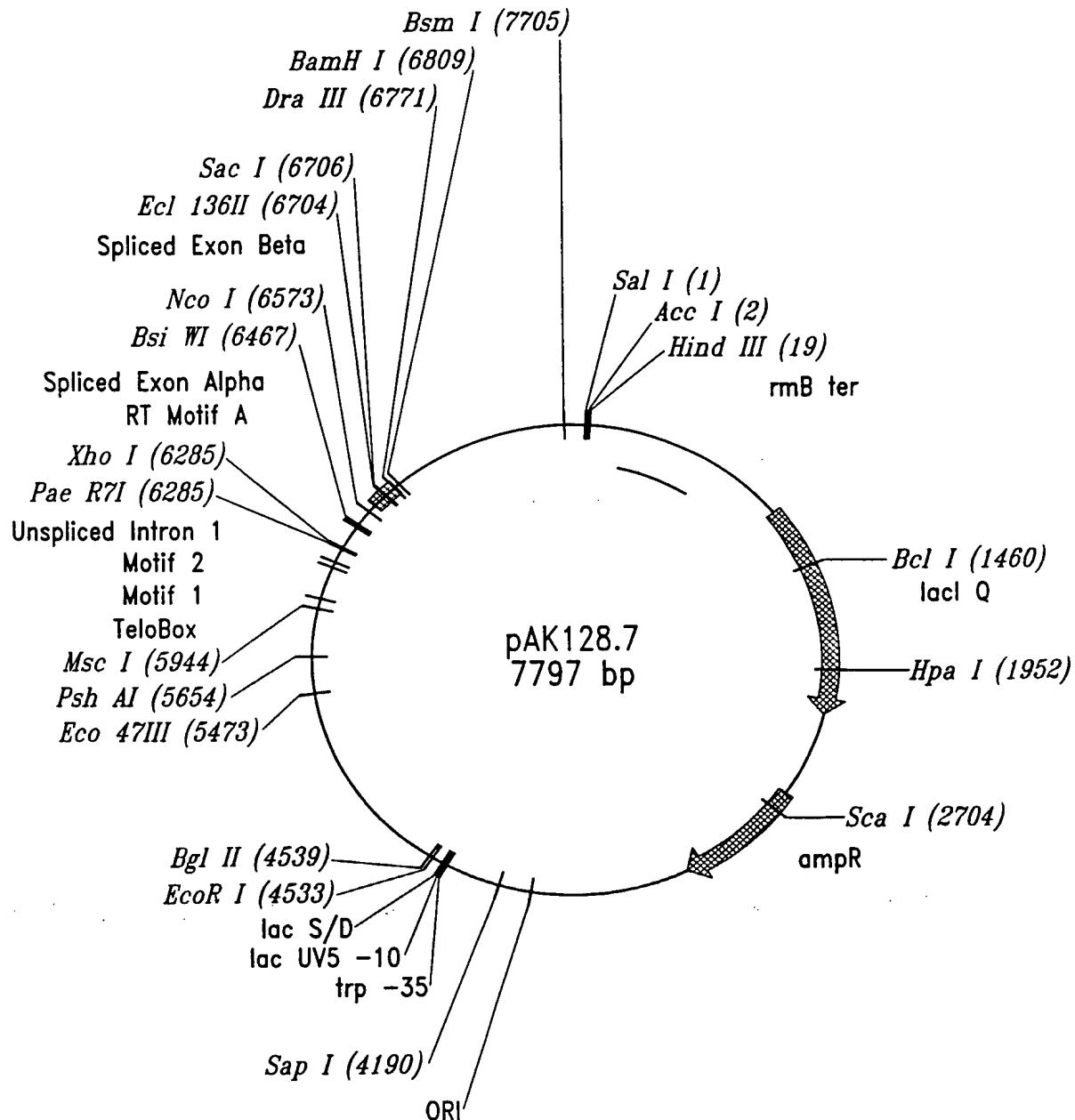


Fig. 14A



LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

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61 aaccctggcg ttacccaact taatcgccct gcagcacatc ccctttcgc cagctggcgt
121 aatagcgaaaggccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
181 tggccctga tgcgttattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
241 tccctgtttt ggcggatgag agaagatttt cagccgtata cagattaaat cagaacgcag
301 aagcggctg ataaaaacaga atttgcctgg cggcagttagc gcgggtgtcc cacctgaccc
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2521 ggttacatcg agaactggat ctcacacgcg gtaagatct tgagatgtttt ccgcggggaa
2581 aacgttttcc aatgtatgagc actttaaag ttctgctatg tggcgcgtt tttatccgtt
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Fig. 14B



2701 agtactcacc agtcacagaa aagcatctta cgatggcat gacagtaaga gaattatgca
2761 gtgctccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcgag
2821 gaccgaagga gctaaccgct ttttgcaca acatggggta tcatgtact cgccttgatc
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Fig. 14C



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Fig. 14D

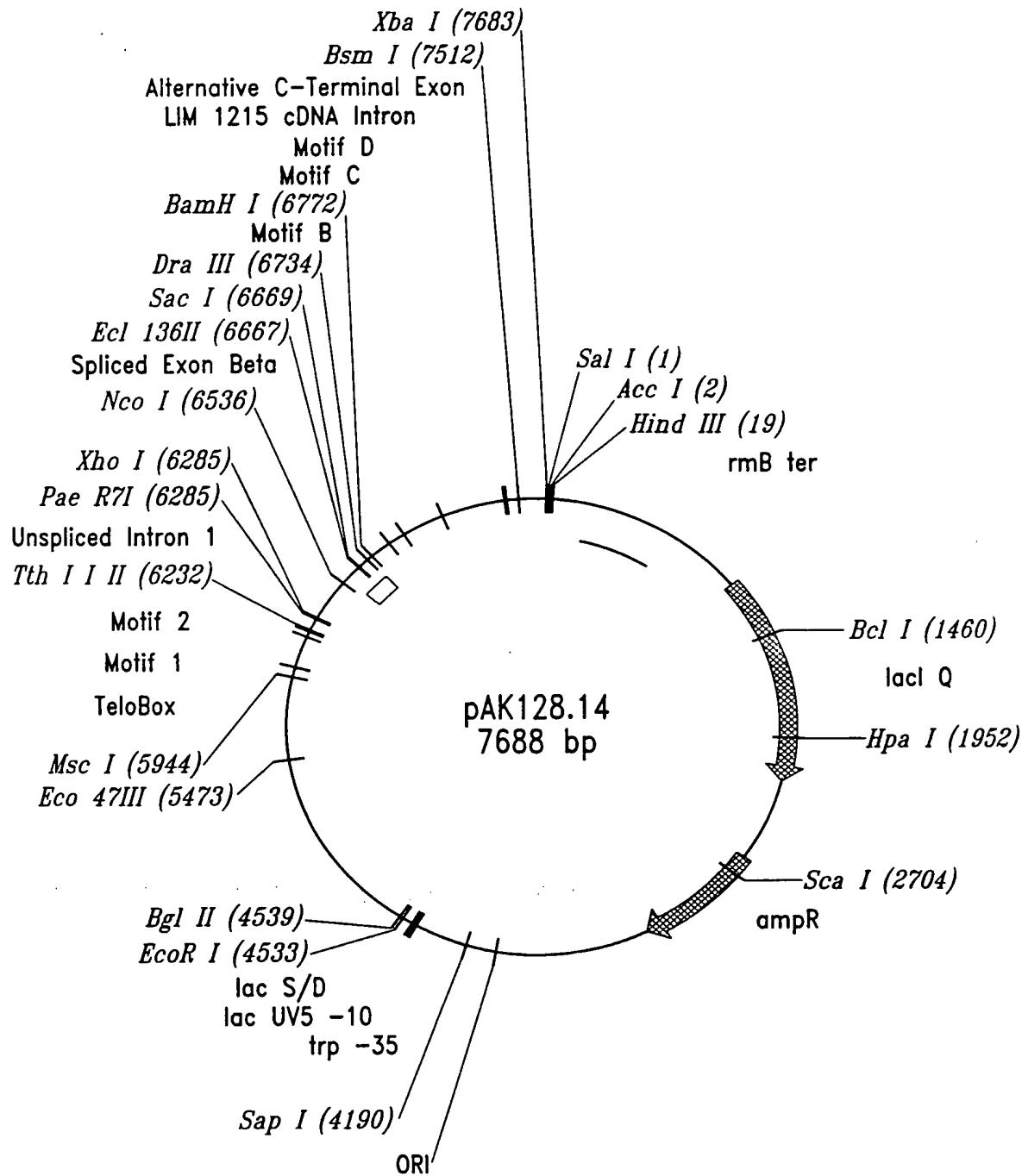


Fig. 15A



LOCUS pAKI28.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

1 tcgacctgca ggcattcaag cttggcactg gccgtcgaaa tacaacgtcg tgactggaa
61 aaccctggcg ttacccaact taatcgccctt gcagcacatc ccccttcgc cagctggcg
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Fig. 15B



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3661 tggctgtgc cagtggcgat aagtcgttgc ttaccgggtt ggactcaaga cgatagttac
3721 cggataaggc gcagcggcgtc ggctgaacgg ggggttcgtc cacacagccc agcttggagc
3781 gaacgaccta caccgaactg agataacctac agcgtgagca ttgagaaaagc gccacgcctc
3841 ccgaaggag aaaggccggac aggtatccgg taagccggcag ggtcggaaaca ggagagcgc
3901 cgagggagct tccagggggaa aacgccttgcg atctttatag tccctgtcggg tttcggccacc
3961 tctgacttgc gctgtcgat ttgtatgtt cgtcagggggg gctggagccata tggaaaaacg
4021 ccagcaacgc ggcctttta cggttcctgg ccttttgcgt gccttttgcgt ccatgttct
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4141 cgcctcgcccg cagccgaacg accgaggcga gcgagtcaatg gagcggagaa gcggaaagagc
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4321 ccatcggaaatgc ctgtggatgc gctgtcgagg tcgtaaatca ctgcataattt cgtgtcgctc
4381 aaggccact cccgttctgg ataattttt ttgcggccgac atcataacgg ttctggcaaa
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4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagt gctgcagagg ctgtgcggc gcccggcggaa gaaacgtcgt gccttcggct
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5041 ggcgtcccc tggccggag cggacggccg ttggccggg gtcctggcc caccggggca
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5341 tgcggccctc cttctactc agtctctga gcccggccgtt gactggccgtt cggaggcgt
5401 tggagaccat ctttctgggt tccaggccctt ggtgcgcagg gactcccccgc aggttgc
5461 gcctggccca ggcgtactgg caaatgcgc cccgtttctt ggagctgtt gggaccac
5521 cgcagtgcggcc ctacgggggtt ctcctcaaga cgcactgcgc gctgcgcgtt gcccggcc

Fig. 15C



5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
5641 aggacacaga ccccccgtcgc ctggtgacgc tgctccgcca gcacagcagc ccctggcagg
5701 tgtacggctt cgtgcgggccc tgccctgcgc ggctggtgcc cccaggcctc tggggctcca
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6241 gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac
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6601 ggcacagtcc tggtgcacc tgcaggagac cagccgcgtg agggatgcgg tcgtcatcga
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6841 gtttgcgggg attcggcggg acgggctgt cctgcgtttt gttggatgatt tcttgggt
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7021 cctgggtggc acggctttt ttcagatgcc ggcccacggc ctattccct ggtgcggcct
7081 gctgctggat accccggaccc tggaggtgca gagcgtactac tccagctatg cccggaccc
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7261 cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acaggttca
7321 cgcatgtgt ctgcagctcc cattcatca gcaaggcttgg aagaacccca cattttcc
7381 ggcgcgtatc tctgacacgg cctccctctg ctactccatc ctgaaaggcca agaaccgagg
7441 gatgtcgctg ggggccaagg ggcgcggccgg ccctctgccc tccgaggccg tgcagtggct
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7681 atctagag

Fig. 15D